

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: January 30, 2006, 08:52:05 ; Search time 45 Seconds  
(without alignments)  
288.446 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 157  
Sequence: 1 YFGKLSKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap.\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	Description
1	156	99.4	US-08-896-605A-6
2	156	99.4	US-08-896-501A-4
3	156	99.4	US-08-884-324-1
4	156	99.4	US-08-996-338-26
5	156	99.4	US-08-558-818-1
6	156	99.4	US-08-974-469A-1
7	156	99.4	US-08-832-180-1
8	156	99.4	US-08-832-198-6
9	156	99.4	US-09-819-902-6
10	156	99.4	US-09-752-510-6
11	156	99.4	US-09-711-899-1
12	156	99.4	US-09-556-972-26
13	156	99.4	US-09-649-063-1
14	156	99.4	US-09-479-862-1
15	156	99.4	US-08-896-605A-2
16	156	99.4	US-08-896-501A-2
17	156	99.4	US-08-832-180-9
18	84	53.5	US-08-982-285-4
19	84	53.5	US-08-982-285-6
20	84	53.5	US-08-982-285-7
21	84	53.5	US-09-700-609-1
22	84	53.5	US-10-105-080-10
23	84	53.5	US-09-775-046-9
24	84	53.5	US-10-100-057-6
25	84	53.5	US-10-100-057-20
26	84	53.5	US-10-100-057-21
27	84	53.5	US-09-398-412B-7

164	2	US-09-949-016-10506	Sequence 10506, A
153	2	US-10-105-080-4	Sequence 4, Appli
153	2	US-09-949-016-6095	Sequence 6095, Ap
157	2	US-08-982-285-11	Sequence 11, Appl
157	2	US-10-100-057-25	Sequence 25, Appl
157	2	US-08-982-285-8	Sequence 8, Appli
157	2	US-10-100-057-22	Sequence 22, Appl
157	2	US-09-597-576-2	Sequence 2, Appli
157	2	US-08-982-285-9	Sequence 9, Appli
157	2	US-10-100-057-23	Sequence 23, Appl
157	2	US-08-832-198-2	Sequence 2, Appli
50	2	US-09-819-902-2	Sequence 2, Appli
50	2	US-09-752-510-2	Sequence 2, Appli
157	2	US-08-982-285-10	Sequence 10, Appl
157	2	US-08-982-285-12	Sequence 12, Appl
157	2	US-10-100-057-24	Sequence 24, Appl
157	2	US-10-100-057-26	Sequence 26, Appl
157	2	US-08-832-198-5	Sequence 5, Appli
17	2	US-09-819-902-5	Sequence 5, Appli
17	2	US-09-752-510-5	Sequence 5, Appli
17	2	US-10-100-057-13	Sequence 13, Appl
17	2	US-08-832-198-4	Sequence 4, Appli
14	2	US-09-819-902-4	Sequence 4, Appli
14	2	US-09-752-510-4	Sequence 4, Appli
14	2	US-10-100-057-12	Sequence 12, Appl
13	2	US-08-832-198-7	Sequence 7, Appli
13	2	US-09-819-902-7	Sequence 7, Appli
13	2	US-09-752-510-7	Sequence 7, Appli
13	2	US-10-100-057-11	Sequence 11, Appl
157	2	US-09-917-265A-5	Sequence 5, Appli
157	2	US-09-917-265A-12	Sequence 12, Appl
179	2	US-09-445-724B-14	Sequence 14, Appl
192	2	US-09-917-265A-8	Sequence 8, Appli
193	2	US-09-445-724B-2	Sequence 2, Appli
193	2	US-09-445-724B-6	Sequence 6, Appli
10	2	US-08-884-324-15	Sequence 15, Appl
10	2	US-08-832-180-7	Sequence 7, Appli
10	2	US-08-832-198-1	Sequence 1, Appli
10	2	US-08-832-198-3	Sequence 3, Appli
10	2	US-09-819-902-1	Sequence 1, Appli
10	2	US-09-819-902-3	Sequence 3, Appli
10	2	US-09-752-510-1	Sequence 1, Appli
10	2	US-09-752-510-3	Sequence 3, Appli
10	2	US-08-982-285-27	Sequence 27, Appl
10	2	US-09-479-862-15	Sequence 15, Appl
10	2	US-10-100-057-10	Sequence 10, Appl
10	2	US-08-558-818-3	Sequence 3, Appli
11	2	US-08-974-469A-3	Sequence 3, Appli
11	2	US-09-711-899-3	Sequence 3, Appli
11	2	US-10-100-057-9	Sequence 9, Appli
133	2	US-09-917-265A-2	Sequence 2, Appli
7	2	US-10-100-057-3	Sequence 3, Appli
46	2	US-08-857-076-83	Sequence 83, Appl
46	2	US-09-205-658-83	Sequence 83, Appl
157	1	US-08-502-538A-2	Sequence 2, Appli
157	1	US-08-908-005A-2	Sequence 2, Appli
157	2	US-08-996-338-27	Sequence 27, Appli
157	2	US-08-558-818-7	Sequence 7, Appli
157	2	US-08-974-469A-7	Sequence 7, Appli
157	2	US-08-832-180-8	Sequence 8, Appli
157	2	US-08-832-198-11	Sequence 11, Appl
157	2	US-09-253-523-2	Sequence 2, Appli
157	2	US-09-251-911-2	Sequence 2, Appli
157	2	US-09-819-902-11	Sequence 11, Appl
157	2	US-09-752-510-11	Sequence 11, Appl
157	2	US-08-982-285-5	Sequence 5, Appli
157	2	US-08-982-285-13	Sequence 13, Appl
157	2	US-08-982-285-14	Sequence 14, Appl
157	2	US-09-711-899-7	Sequence 7, Appli
157	2	US-09-556-972-27	Sequence 27, Appl
157	2	US-09-700-609-2	Sequence 2, Appli
157	2	US-09-649-063-2	Sequence 2, Appli

## ALIGNMENTS

## RESULT 1

US-08-896-605A-6  
; Sequence 6, Application US/08896605A  
; Patent No. 5879942  
; GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 18 JULY 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 207,691/1996  
; FILING DATE: 19-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 156,062/1997  
; FILING DATE: 30-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TANIMOTO=2  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-896-605A-6

Query Match 99.4%; Score 156; DB 1; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMKQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMKQFESSY 120  
Qy 121 EGYFLACEKERDLFKLILKXKDELDGRSMTFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKXKDELDGRSMTFTVQNE 157

## RESULT 2

US-08-896-501A-4  
; Sequence 4, Application US/08896501A  
; Patent No. 5891663  
; GENERAL INFORMATION:

APPLICANT: TANIMOTO, Tadao  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 18-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 213,267/1996  
FILING DATE: 25-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 31,474/1997  
FILING DATE: 31-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TANIMOTO=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-896-501A-4

Query Match 99.4%; Score 156; DB 1; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60  
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMKQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQRSVPVGHDKMKQFESSY 120  
Qy 121 EGYFLACEKERDLFKLILKXKDELDGRSMTFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKXKDELDGRSMTFTVQNE 157

## RESULT 3

US-08-894-324-1  
; Sequence 1, Application US/08884324  
; Patent No. 6060283  
; GENERAL INFORMATION:  
; APPLICANT: Takanori OKURA  
; APPLICANT: Kakuji TORIGOE  
; APPLICANT: Masahi KURIMOTO  
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
; OF INDUCING THE PRODUCTION OF INTERFERON-  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington

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STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-884-324-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISKLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISKLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157

RESULT 4
US-08-996-338-26
Sequence 26, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185,305/96
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-884-324-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISKLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISKLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
```

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TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
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RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KENKYUJO
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: TORIGOE, Kakui
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=1A
```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
US-08-832-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KENKYUJO
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: USHIO, Shimpei
APPLICANT: TORIGOE, Kakui
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-832-180-1

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDNKKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDNKKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsujiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-832-198-6

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDNKKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQFORSVPGHDNKKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 9
US-09-819-902-6
; Sequence 6, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsujiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09/09/819,902
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
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TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'Ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-819-902-6

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-09-752-510-6
; Sequence 6, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuaki
; TANIMOTO, Tadao
; KURIMOTO, Masaashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-Jan-2001
; APPLICATION NUMBER: US/09/752,510
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; 'Ile' or 'Thr'
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-752-510-6

Query Match          99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.2e-157;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11
US-09-711-899-1
; Sequence 1, Application US/09711899
; Patent No. 6509449
; GENERAL INFORMATION:
; APPLICANT: <Unknown>
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/711,899
; FILING DATE: 13-No. 6509449-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,818
; FILING DATE: 2000-11-15
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-711-899-1
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Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 12  
US-09-556-972-26  
; Sequence 26, Application US/09556972  
; Patent No. 6559298  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; OKURA, Takanori  
; KURIMOTO, Musashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/556,972  
; FILING DATE: 24-Apr-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,338  
; FILING DATE: 22-DEC-1997  
; APPLICATION NUMBER: JP 74,697/1997  
; FILING DATE: 12-MAR-1997  
; APPLICATION NUMBER: JP 215,488/1997  
; FILING DATE: 28-JUL-1997  
; APPLICATION NUMBER: JP 291,837/1997  
; FILING DATE: 09-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE=3  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-556-972-26

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120

DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 13  
US-09-649-063-1  
; Sequence 1, Application US/09649063  
; Patent No. 6600022  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; USHIO, Shimpel  
; KUNIKATA, Toshio  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/649,063  
; FILING DATE: 29-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/996,140  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: JP 52,526/1997  
; FILING DATE: 21-FEB-1997  
; APPLICATION NUMBER: JP 163,490/1997  
; FILING DATE: 6-JUN-1997  
; APPLICATION NUMBER: JP 215,490/1997  
; FILING DATE: 28-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE=2  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-649-063-1

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHNDKMQFESSY 120

Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 157  
RESULT 14  
US-09-479-862-1  
; Sequence 1, Application US/09479862  
; Patent No. 6790442  
; GENERAL INFORMATION:  
; APPLICANT: Takatori OKURA  
; APPLICANT: Kakuji TORIGOE  
; APPLICANT: Masahi KURIMOTO  
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/479,862  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/894,324  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: OKURA=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-479-862-1  
Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8.2e-157;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 157  
RESULT 15  
US-08-896-605A-2  
; Sequence 2, Application US/08896605A  
; Patent No. 5879942

; GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/896,605A  
; FILING DATE: 18 July 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 207,691/1996  
; FILING DATE: 19-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 156,062/1997  
; FILING DATE: 30-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TANIMOTO=2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-896-605A-2  
Query Match 99.4%; Score 156; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. 1e-156;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKQFESSY 120  
Db 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKKQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 157  
Db 157 EGYFLACEKERDLFKLILKKEDELGRSIMFTVQNE 193  
RESULT 16  
US-08-896-501A-2  
; Sequence 2, Application US/08896501A  
; Patent No. 5891663  
; GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.



COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/896,501A  
FILING DATE: 18-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 213,267/1996  
FILING DATE: 25-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 31,474/1997  
FILING DATE: 31-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TANIMOTO-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-896-501A-2

Query Match 99.4%; Score 156; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. le-156;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120  
DB 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 17  
US-08-832-180-9  
Sequence 9, Application US/08832180  
Patent No. 6214584  
GENERAL INFORMATION:  
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU  
APPLICANT: KENYUJO  
APPLICANT: USHIO, Shimei  
APPLICANT: TORIGOE, Kakuji  
APPLICANT: TANIMOTO, Tadao  
APPLICANT: OKAMURA, Haruki  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING  
TITLE OF INVENTION: POLYPEPTIDE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/832,180  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/558,191  
FILING DATE:  
APPLICATION NUMBER: JP 304,203/94  
FILING DATE: No. 6214584ember 15, 1994  
APPLICATION NUMBER: 10048102  
FILING DATE: September 18, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: USHIO=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-832-180-9

Query Match 99.4%; Score 156; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. le-156;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 120  
DB 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSVPGHNDKMQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 18  
US-08-982-285-4  
Sequence 4, Application US/08982285  
Patent No. 6476197  
GENERAL INFORMATION:  
APPLICANT: YAMAMOTO, Koza  
APPLICANT: OKAMOTO, Iwao  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 7th Street N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/982,285  
FILING DATE:  
PRIOR APPLICATION DATA:

..

Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKERDL 133  
Qy 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 21  
US-09-700-609-1  
; Sequence 1, Application US/09700609  
; Patent No. 6582689  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Randall K  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: P50777  
; CURRENT APPLICATION NUMBER: US/09/700,609  
; CURRENT FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/086,560  
; PRIOR FILING DATE: 1999-05-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Human  
US-09-700-609-1

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKERDL 133  
Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKERDL 133  
Qy 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 22  
US-10-105-080-10  
; Sequence 10, Application US/10105080  
; Patent No. 6800479  
; GENERAL INFORMATION:  
; APPLICANT: SAMYANG GENEX CORPORATION  
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/105,080  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: KR 10-2001-78296  
; PRIOR FILING DATE: 2001-12-11  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 10  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Human mature interleukin-18 mutant  
US-10-105-080-10

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKERDL 133  
Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKERDL 133  
Qy 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 23  
US-09-775-046-9  
; Sequence 9, Application US/09775046  
; Patent No. 6843987  
; GENERAL INFORMATION:  
; APPLICANT: Debets, Johannes Eduard Maria Antonius  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS  
; FILE REFERENCE: DX01073K  
; CURRENT APPLICATION NUMBER: US/09/775,046  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/179,638  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-046-9

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKERDL 133  
Db 74 LSCENKIISFKEMPPDNKDKTSIIFFQRSVPGHDKMKQFESSSYEGYFLACEKERDL 133  
Qy 134 FKILKKEDELGDRSIMFTVQNE 157  
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 24  
US-10-100-057-6  
; Sequence 6, Application US/10100057  
; Patent No. 6896880  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; HORWOOD, Nicole Joy  
; UDAGAWA, No. 6896880yuki  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE=1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
DB 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKLILKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLILKKEDELGDRSIMFTVQNEED 157

RESULT 25  
US-10-100-057-20  
Sequence 20, Application US/10100057  
Patent No. 6896880  
GENERAL INFORMATION:  
APPLICANT: GILLISPIE, Matthew Todd  
HORWOOD, Nicole Joy  
UDAGAWA, No. 6896880yuyuki  
KURIMOTO, Masashi  
TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/10/100,057  
FILING DATE: 19-Mar-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,061  
FILING DATE: 25-FEB-1998  
APPLICATION NUMBER: JP 55,468/1997  
FILING DATE: 25-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GILLISPIE=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-100-057-20

Query Match 53.5%; Score 84; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 9e-81;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
DB 74 LSCENKIISFKEMNPPDNIKDKSDIIFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKLILKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLILKKEDELGDRSIMFTVQNEED 157

Search completed: January 30, 2006, 08:59:52.  
Job time : 45 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:30:42 ; Search time 39 Seconds  
(without alignments)  
387.334 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLSVIRNLDQVL.....LKKDELGDRSIMFTVQNEED 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 80:\*

1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	515	63.4	192	2 S60226	cytokine IGIF - mo
2	85	10.5	381	2 T40341	hypothetical prote
3	82	10.1	263	2 T39487	hypothetical prote
4	81.5	10.0	270	1 S10532	interleukin-1 alph
5	80.5	9.9	866	2 C71509	probable DNA polym
6	79	9.7	452	2 D64583	hypothetical prote
7	78.5	9.7	204	2 T44357	hypothetical prote
8	78	9.6	473	2 T32038	hypothetical prote
9	77.5	9.5	1251	2 A56677	neuronal cell cycl
10	77	9.5	364	2 A81261	probable periplasm
11	76	9.4	632	2 T00679	hypothetical prote
12	76	9.4	747	2 E84698	hypothetical prote
13	75.5	9.3	192	2 S15661	(2'-5')oligo(A) sy
14	75.5	9.3	270	2 I46620	interleukin-1 alph
15	75.5	9.3	1036	2 H64245	hypothetical prote
16	75.5	9.3	1663	1 C3MS	complement C3 prec
17	75	9.2	1064	1 S57450	protein-tyrosine k
18	75	9.2	2470	2 I50726	cation-independent
19	74.5	9.2	334	2 T04198	hypothetical prote
20	74.5	9.2	389	2 B69277	TRK potassium upre
21	74.5	9.2	467	2 A48713	serine/threonine-s
22	74.5	9.2	1228	2 A57384	multimerin, endoth
23	74.5	9.2	1510	2 T16927	hypothetical prote
24	74	9.1	245	2 B30488	hypothetical prote
25	74	9.1	361	2 E36904	mand family ATPase
26	74	9.1	376	2 T24925	hypothetical prote
27	74	9.1	467	2 I49609	proto-oncogene pro
28	74	9.1	467	2 A47388	serine/threonine p
29	74	9.1	680	2 A28121	major merozoite su

virb4 protein prec  
major merozoite su  
probable small sub  
probable small sub  
seryl-tRNA synthet  
hypothetical prote  
interleukin-1 alph  
protein F27J15.10  
polynucleotide ade  
hypothetical prote  
p101 protein precu  
probable membrane  
DNA helicase II BR  
EIN2 protein - Ara  
hypothetical prote  
protein BRG1 - hum  
interleukin-1 alph  
hypothetical prote  
weakly probable su  
conserved hypotet  
nodulin / glutamat  
ABC transporter, A  
probable type II D  
Mrs2p [imported] -  
hypothetical prote  
gene cel IF A3 pro  
No-on-transient A  
No-on-transient A  
erythrocyte membra  
hypothetical prote  
interleukin-1 alph  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
minor outer capsid  
hypothetical prote  
magnesium and coba  
hypothetical prote  
glycosyltransferas  
hypothetical prote  
hypothetical prote  
hypothetical prote  
SNF2beta protein -  
interaptin - slime  
centromere translati  
probable translati  
hypothetical prote  
hypothetical prote  
biotin carboxylase  
phytoene dehydroge  
hypothetical prote  
hypothetical prote  
DNA-directed RNA p  
conserved hypotet  
hypothetical prote  
hypothetical prote  
ATP-dependent RNA  
starch synthase ho  
interleukin-1 alph  
hypothetical prote  
conserved hypotet  
isopenicillin N sy  
isopenicillin N sy  
conserved hypotet  
conserved hypotet  
fes oxidoreductase  
hypothetical prote  
Hsp90 homolog pei  
hypothetical prote  
hypothetical prote  
uncharacterized pr

## ALIGNMENTS

```
RESULT 1
S60226
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torigoe,
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009; PMID:7477296
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OKA>
A:Cross-references: UNIPROT:P70380; UNIPARC:UPI00000019DE; EMBL:D49949; NID:g1064822; P
C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.4%; Score 515; DB 2; Length 192;
Best Local Similarity 64.9%; Pred. No. 8.3e-42;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

Qy 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIFIISMYKDSQPRGMA 61
Db 37 FGRLLHCTTAVIRNLNDQVLFVDK-RQVFVEDMTDIDQASSEPQTRLLIYMYKDSVGRGLA 95

Qy 62 VTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTKSDIIFQSRVPGHDKMKQPFSSSYE 121
Db 96 VTISVKDSKNTSLCKKNIISFKEMDPENIDDIQSDLIIFQKRVPGH-NKMEFESSLYE 154

Qy 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 155 GHFLACQKEDAFKLLKXKXDKNGSKVMFTLN 188

*RESULT 2
T40341
hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40341
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z21922
A:Accession: T40341
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-381 <WOO>
A:Cross-references: UNIPROT:O43031; UNIPARC:UPI0000006C88A; EMBL:AL022070; PIDN:CAA17782.
A:Experimental source: strain 972h-; cosmid c3B9
C:Genetics:
A:Gene: SPDB:SPBC3B9.02c
A:Map position: 2

Query Match 10.5%; Score 85; DB 2; Length 381;
Best Local Similarity 26.4%; Pred. No. 1.8;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;

Qy 3 GKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIFIISMYKDSQPRGMAV 62
Db 208 GOLSSKDAF--DYNQRTFLGMAKPYDSELTEDIWKNPKKTMF-----250

Qy 63 TISVK-CEKISXLSCEKNIISF-KEMNPPDNIDKTKSDIIFQSRVPGHDKMKQPFSSSY 120
Db 251 -LPVKPLESNALNSQNEHTEVQKNSIDNL--TFSSSELFRRKS---RDNNLSRESS-- 302

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRS 148
Db 303 -----VSSKLDYNSRNNKRRDRDPRT 325
```

```
RESULT 3
T39487
hypothetical protein SPBC15D4.11c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39487
R:lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21858
A:Accession: T39487
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-263 <LYN>
A:Cross-references: UNIPROT:O74316; UNIPARC:UPI0000006ABF8; EMBL:AL031349; PIDN:CAA20486
A:Experimental source: strain 972h-; cosmid c15D4
C:Genetics:
A:Gene: SPDB:SPBC15D4.11c
A:Map position: 2
A:Introns: 96/2; 147/3
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;
Best Local Similarity 21.7%; Pred. No. 2.3;
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;

Qy 4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIFIISMYKDSQPRGMAV 63
Db 47 KLDSELGVYKQVLDLTPKKGYEKALHSFIHED-----PSLNYISALKETAKERIRVT 100

Qy 64 ISVKCEKISXLSCEKNIISFKEMNPPDNIDKTKSDIIFQSRVPGH-----109
Db 101 VPIVSRKSYV--QTRPIHTSAEN--ENGNETSDLVFFQHSIPAYVQVLTNNHGTILCAL 156

Qy 110 ---DNMKQPFSSSYEGYFLACEKERDLFKLILKKEDELGDR 147
Db 157 ILCKGMLHFDLSIFQSPQNSQAFSSDL-RLILQKSQKYTGR 196

RESULT 4
S10532
interleukin-1 alpha precursor - pig
N:Alternate names: hematopoietin-1; IL-1 alpha
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-Feb-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S10532
R:Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.B.
Nucleic Acids Res. 18, 4282, 1990
A:Title: Porcine IL-1 alpha cDNA nucleotide sequence.
A:Reference number: S10532; MUID:90332454; PMID:2377484
A:Accession: S10532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <MAL>
A:Cross-references: UNIPROT:P18430; UNIPARC:UPI000012D493; EMBL:X52731; NID:g1987; PIDN
C:Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte pro
C:Comment: IL-1 proteins are involved in the inflammatory response, being identified as
118.
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleava
ved form of interleukin-1alpha, unlike interleukin-1beta, is fully active.
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macropha
F:112/Domain: propeptide #status predicted <PRO>
F:113-270/Product: interleukin-1 alpha #status predicted <full>
F:82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 2.6;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

Qy 8 KLSVIRNLNDQVLFIDQGNRPLFEDMTD----SDCRDNAPRTI-FIISMYKDSQPRGMAV 62
```

```

Db      123 KYNFWRVINHQICLLNDARNQSIIRPSGOYLMAAVLNLDKAVKFDMAAYTENDOSQLPV 182
Qy      63 TISVKCEKISXLSCEN--KLSFKEM-NPPDNIKOTKSDIIIFQSRVPGHDNNMQFESS 119
Db      183 TLRIS-ETRLFVSAQNEDEVLLKELPTPTKIKDETSLLFWEK-----HGNMDYFKSAA 237
Qy      120 YEGYFLACEKER 131
Db      238 HPKLFIAIATRQEK 249

```

RESULT 5  
C71509  
probable DNA polymerase I, Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: C71509  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra  
A:Reference number: A71570; MUID:99000809; PMID:9784136  
A:Accession: C71509  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-866 <RN>  
A:Cross-references: UNIPROT:O84500; UNIPARC:UPI000000D3352; GB:AE001322; NID  
A:X:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: polA  
C:Superfamily: DNA-directed DNA polymerase I

RESULT 6  
D64583  
hypothetical protein HP0508 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: D64583  
R:Tomb, J.F.; White, O.; Kervlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Frazer, C. A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A6520, MUID:97394467; PMID:9252185  
A:Accession: D64583  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-452 <TOM>

```
Query Match          9.7%; Score 79; DB 2; Length 452;
Best Local Similarity 23.8%; Pred. No. 8.3;
Matches 40; Conservative 30; Mismatches 72; Indels 26; Gaps 8;
```

Db LVTFRFNQQA-FLIAPNDELYEGRATNTDINFISSDLLVTFLNGFPDKIANLRKACNV 163

QY 59 -GMATVTSVCKEKISXLSCEN-KIISPKEMNPPDNIKDTKSDIIFQFORSVPGHD----NK 112

Db 164 YSGVGIYIVTTNTINILSCSFSEILEKREL---DTSGVTKTSTPPFSR-VEGIDAGTLGK 219

QY 113 MQFESISYEGYF---LACEKERDLFKLILKKEDELDGRSIMFTVONE 156

Db 220 L-FSGSOKNYFAYDALVKRKEKVEYIKKREKIDSRFKRETKOF 266

```

RESULT 7
T44357
hypothetical protein [imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44357
R:Matsumita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.
J. Bacteriol. 181, 923-933, 1999
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum
A:Reference number: Z22752; MUID:99121032; PMID:9922257
A:Accession: T44357
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-204 <MAT>
A:Cross-references: UNIPROT:Q9ZNU7; UNIPARC:UPI00000B182D; EMBL:AB014075; NID:G3868863
A:Experimental source: strain JCM 1403

```

```

Query Match          9.7%; Score 78.5; DB 2; Length 204;
Best Local Similarity 26.4%; Pred. No. 3.6;
Matches 32; Conservative 19; Mismatches 51; Indels 19; Gaps 5;

QY      9  LSVIRNLNDQVLFDIDCGNRLFFEDMTDSDCRDNAPRTIFII--SMYKDSQPRGMAVTISV 66
DB      25  ISTFENRHHKASNGKQGEAKTGBKIN---IDNSSSIKIVYESVYLKPEGEQNKTTVDE 80

QY      67  KCEK-----ISXLSCEKNKIIISFKEMNPPDNIKDKSDIIFORSVPFGHDKMKOFESSS 119
DB      81  CLEKFNKDKKVISDMTKEQVLAVFKKHD--YNLKDICKDQIVFSESI---NKYKYQEGK 134

QY      120  Y 120
DB      135  Y 135

```

RESULT 8  
T32038  
hypothetical protein F41B5.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T32038  
R:Dante, M.; Kramer, J.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid F41B5.  
A:Reference number: Z2115  
A:Accession: T32038  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-473 <DAN>  
A:Cross-references: UNIPROT:O16673; UNIPARC:UPI0000080265; EMBL:AF016676; PIDN:AAC2590  
A:Experimental source: strain Bristol N2; clone F41B5  
C:Genetics:

Query Match	9.6%	Score 78	DB 2	Length 473
Best Local Similarity	21.5%	Pred. No. 11		
Matches 32	Conservative 28	Mismatches 57	Indels 32	Gaps 6

```
QY 10 SVIRNLNDQVLF---IDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGMATISV 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 NALANVINQITFGYRFDESNOEYKXKH-----LIEFOENVFTSAKVTVQV 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 KCEKISLSCENKIISFKENPNPDNIKOTKSDII-PQRSVPQHDNKMQFESSSYEGYFL 125
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 FAPKL-----GKILGESLE--DLMKWKNFYDFNTQIENHROKIDFDSSESDYAE 268
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 126 ACKERDLFKLILKKEDELGDRSIMFTVQ 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 AYLKEQ-----KKYEALGDTLFSNKQ 290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
A56677
neural cell cycle withdrawal protein QW1 - quail (fragment)
C:Species: Coturnix coturnix (quail)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C:Accession: A56677
R:Bidou, L.; Crisanti, P.; Blancher, C.; Pessac, B.
Mech. Dev. 43, 159-173, 1993
A:Title: A novel cDNA corresponding to transcripts expressed in retina post-mitotic neu
A:Reference number: A56677; MUID:94128599; PMID:8297788
A:Accession: A56677
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1251 <BID>
A:Cross-references: UNIPROT:O91365; UNIPARC:UPI00000FB847; GB:S68151; NID:G545153; PIDN:
A>Note: conceptual translation not given

Query Match 9.5%; Score 77.5; DB 2; Length 1251;
Best Local Similarity 23.5%; Pred. No. 38;
Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps 9;

QY 6 ESLSVI-RNLNDQVLF---DQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGMA 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 EEKLAIQKEMDEQVIOGYQENELRYKQMKDLQIQNKNEE-----QMYKENQCL-MS 702
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VITSVKCEKISLSCENKIISFKENPNPDNIKOTKSDIIFFQRSVPQHDNKMQF----- 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 703 ELIALR-EKVERINIOSQIV--RESEPARN--QSFTELISELGAARKEETKLEERIRLK 757
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 --SSSYEGVFLACEKRDLPKILKKEDELGDRSIMFTVQNE 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 758 QDKQALELDLQAKKERDLAKVQITSTS--SEKSYBFKIMEE 797
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
A81261
probable periplasmic protein Cjl643 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81261
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: A81261
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <PAR>
A:Cross-references: UNIPROT:Q9PM33; UNIPARC:UPI00000C1FAB; GB:A1111169; NID
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cjl643

Query Match 9.5%; Score 77; DB 2; Length 364;
Best Local Similarity 24.8%; Pred. No. 9;
Matches 38; Conservative 21; Mismatches 40; Indels 54; Gaps 9;

QY 12 IRNLNDQVLFIDQGNRPLFEDMTDSDCRD-NAPRTIFIISMYSK-----DSQPR----- 58
```

```
Db 211 LRKLNKELFLDARGSTLYFQVLRDN--MDLNISTEVFAKUSKFNLPDSKPKPKTNTFTS 268
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 --GMAVTISVKCEKI-----SXLSCENKII-SFKEMNPPDNI----- 92
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 NLGLTVNASLVVTKIDPKSKVSNAGFMVGDKILRVNNILANNFKEL---QNILSAGNDFS 325
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 93 -----KOTKSDIIFFQRSVPQH-----DNKMQF 115
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 326 ILIERKSTKLPLSNFNNELGGNANSGGDGKQFQ 358
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
T00679
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F6E13.12
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00679; A84873
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A:Reference number: Z14180
A:Accession: T00679
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-632 <ROU>
A:Cross-references: UNIPROT:O80569; UNIPARC:UPI00000A05B0; EMBL:AC004005; NID:G3212846;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84873
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-632 <STO>
A:Cross-references: UNIPARC:UPI00000A05B0; GB:AE002093; NID:G3212856; PIDN:AAC23407.1;
C:Genetics:
A:Gene: At2g43990; F6E13.12
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 632;
Best Local Similarity 25.6%; Pred. No. 24;
Matches 34; Conservative 29; Mismatches 40; Indels 30; Gaps 9;

QY 28 PLFEDMTDSD-CRDNAPRTIFIISMYSKDSQPRGMATISVKCEK-----ISXLSCENK 79
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 PLSDRSASSDLQNISSGSLSPMDIYKETTR---ISSLSNPLFRFRFHLSSCDGE 424
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 IISFK-----EMNPPDNIKTKSDIIFFQRSVP--GHDNKMQF--ESSSYEGYF-LACEK 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 ASAPDTSPTCELDPEHLKDGKSSPL----SVDTLGSENVIQTPESNSFDNYFGLSCSQ 480
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 ERDLFKLILKKEDEL 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 AE-----IQKKHD 488
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
E84698
hypothetical protein At2g29620 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84698
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
```



A;Accession: B94698  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1747 <STO>  
A;Cross-references: UNIPROT:O82393; UNIPARC:UPI000009F050; GB:AE002093; NID:g3582336; PID:146620  
C;Genetics:  
A;Gene: At2g29620  
A;Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 747;  
Best Local Similarity 24.7%; Pred. No. 29;  
Matches 36; Conservative 29; Mismatches 59; Indels 22; Gaps 7;  
QY 4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMATV 63  
DB 102 KKHQOSVVRNARKV-----EVGKQWDSQASEDERGKVLTLLTYGEVLPE---T 150  
QY 64 ISVCKEKISXLSKCNKIIFKEMNPPDNKDKTSDIFFQR--SVPGHDKMKQFE---SS 118  
DB 151 ITPDMEKFK-----RENTLLVAEENVFDSVLDNRDLVLERLISVDG--DDESEVCSSS 205  
QY 119 SYEGYFLACEKERDIFKLIK-KEDE 143  
DB 206 SSEGEKEEEREDVSKVYVAWTEDD 231

RESULT 13  
S15661  
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1993 #sequence\_revision 02-Jun-1994 #text\_change 09-Jul-2004  
A;Accession: S15661; S19108  
R;Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.  
Nucleic Acids Res. 19, 1917-1924, 1991  
A;Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked genes  
A;Reference number: S15660; MUID:91232962; PMID:1709495  
A;Accession: S15661  
A;Molecule type: mRNA  
A;Residues: 1-192 <RUT>  
A;Cross-references: UNIPROT:O60856; UNIPARC:UPI000017629F; EMBL:X55982  
R;Williams, B.  
submitted to the EMBL Data Library, September 1990  
A;Reference number: S19108  
A;Accession: S19108  
A;Molecule type: mRNA  
A;Residues: 1-175, 'L', 177-192 <WIL>  
A;Cross-references: UNIPARC:UPI0000028771; EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:146620  
C;Superfamily: oligo(A) synthetase  
C;Keywords: nucleotidyltransferase

Query Match 9.3%; Score 75.5; DB 2; Length 192;  
Best Local Similarity 23.2%; Pred. No. 6.5;  
Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;  
QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKD 54  
DB 11 GRSDADLVFVNLTSTFEDQNLQOQVLKEIKKQCEVQHERRC----- 54  
QY 55 SQPRGMATVISVKCEKISXLSKCNKIIFKEMNPPDNKDKTSDI----- 100  
DB 55 -----GVKFEVHSLRSPNSRALSFK-LSAPDLLKEVFDVLPAYDLLDHLNLIK 103  
QY 101 -----FFQR---SVP-GHDKMKQFESSYEGYFLACE---KERDLFKLI-----LKEDELG 145  
DB 104 PNQOFYANLTSGVPAGKEGKLSICFMGLQKYFLNCRPTKLRRLRLVTHWYQLCKE-KLG 162  
QY 146 D 146  
DB 163 D 163

RESULT 14  
I46620

interleukin-1 alpha precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
A;Accession: I46620  
R;Maliszewski, C.  
Nucleic Acids Res. 14, 4282, 1990  
A;Title: Nucleotide sequence of porcine interleukin-1 alpha.  
A;Reference number: I46620  
A;Accession: I46620  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-270 <MAL>  
A;Cross-references: UNIPROT:P18430; UNIPARC:UPI000014F113; GB:M86730; NID:g164622; PID:146620  
C;Superfamily: interleukin-1  
C;Keywords: lipoprotein; myristylation  
F;1-112/Domain: propeptide #status predicted <PRO>  
F;113-270/Product: interleukin-1 alpha #status predicted <IL1>  
F;82.83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 9.3%; Score 75.5; DB 2; Length 270;  
Best Local Similarity 22.0%; Pred. No. 9.7;  
Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;  
QY 8 KLSVIRNLNDQVLFIDQGNRPLFEDMTD---SDCRDNAPRTI-FIISMYKDSQPRGMATV 62  
DB 123 KYNFMRVINHOCLINDARNOSIIRDPGQVLMAAVLNLANLDEAVKFDMAAYTSNDDSQLPV 182  
QY 63 TISVKCEKISXLSKCN--KIISFKEM--NPPDNKDKTSDIFFQSVPGHDKMKQFESS 119  
DB 183 TLRTS-ETRLFVSAQNEDEPVLKELPETPKTKIDETSLFFWEK---HGNMDFKSA 237  
QY 120 YEGYFLACEKER 131  
DB 238 HPKLLIATROEK 249

RESULT 15  
H64245  
hypothetical protein MG414 - Mycoplasma genitalium  
C;Species: Mycoplasma genitalium  
C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
A;Accession: H64245; G64245  
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.  
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A;Title: The minimal gene complement of Mycoplasma genitalium.  
A;Reference number: A64200; MUID:96026346; PMID:7569993  
A;Accession: H64245  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1036 <TIG>  
A;Cross-references: UNIPROT:P47653; UNIPARC:UPI0000139789; GB:U39727; GB:L43967; NID:g1046127; PID:g1046127  
A;Experimental source: strain G-37  
A;Accession: G64245  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 'M', 310-1036 <TIG2>  
A;Cross-references: UNIPARC:UPI0000178CFC; GB:U39727; GB:L43967; NID:g1046127; PID:g1046127  
A;Experimental source: strain G-37  
C;Genetics:  
A;Genetic code: SGC3  
A;Start codon: GTG  
C;Superfamily: hypothetical protein MG413

Query Match 9.3%; Score 75.5; DB 2; Length 1036;  
Best Local Similarity 21.9%; Pred. No. 47;  
Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;  
QY 14 NLNDQVLFIDQGNRPLFED---MTSDCRDNAPRTIFIISMYKDSQPRGMATVISVKCEK- 70  
DB 845 SLNDEQLLVLDKLNITLSEKRLQTTKNVFNKNKFNHLENKQFNLFVDVDSKSL 904

```

Qy 71 -ISXLSKENIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMOPFESSSYEGYFLACEK 129
Db 905 FIKGVNDNQVFSISY-----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950
Qy 130 ERDLFKLI---LKKEDLGDRSIMEVONED 157
Db 951 QTQLFKALSFYLKONNLQFKRVPDFNLKSQD 981

```

Search completed: January 30, 2006, 08:41:03  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:29:42 ; Search time 161 Seconds

(without alignments)  
688.000 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLVRLNDQVL.....LKKEDELGDRSMTFTQVED 157

Scoring table: BLOSUM62 , Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	189	2	Q6WJ7 HUMAN
2	811	99.9	193	1	IL18 HUMAN
3	811	99.9	193	2	Q6FGY3 HUMAN
4	798	98.3	193	2	Q96KJ8 HUMAN
5	792	97.5	193	2	Q9BG15 MACMU
6	659	81.2	193	1	IL18 HORSE
7	659	81.2	193	2	Q6TLW4 BUBBU
8	659	81.2	193	2	Q6T573 BUBBU
9	654	80.5	178	2	Q9WZL8 BOVIN
10	654	80.5	193	1	IL18 BOVIN
11	651	80.2	193	2	Q5I931 BOSTR
12	648	79.8	193	2	Q9GL09 SHEEP
13	647	79.7	159	2	Q6QVCA CAPHI
14	637	78.4	192	1	IL18 PIG
15	634	78.1	192	2	Q9SM33 FELCA
16	633	78.0	192	2	Q865B8 FELCA
17	626	77.1	192	2	Q9N1P7 PIG
18	613	75.5	193	1	IL18 CANPA
19	578	71.2	177	2	Q6STL7 PIG
20	536.5	66.1	195	2	Q80Y07 MERUN
21	515	63.4	189	2	Q9OSS8 MOUSE
22	515	63.4	192	1	IL18 MOUSE
23	514.5	63.4	194	1	IL18 RAT
24	511.5	63.0	194	2	Q541E6 RAT
25	501	61.7	192	2	Q6USQ6 MOUSE
26	441	54.3	196	2	Q91Z66 SIGHI
27	313	38.5	84	2	Q95LE7 CANFA
28	293	25.1	45	2	Q9NQ49 HUMAN
29	194	23.8	211	2	Q98SQ1 ANAPL
30	184.5	22.7	196	2	Q6IT44 CHICK
31	184.5	22.7	198	2	Q8AV26 MELGA

32	182.5	22.5	198	2	Q9I8D2 CHICK
33	178.5	22.0	196	1	IL18 CHICK
34	174.5	21.5	198	2	Q5S4P2 CHICK
35	116	14.3	199	2	Q70PK1 ONCMY
36	111	13.7	182	2	Q6EV48 ONCMY
37	111	13.7	199	2	Q6EV49 ONCMY
38	94.5	11.6	1408	2	Q4S1M3 TETNG
39	88.5	10.9	357	2	Q5BD42 EMENI
40	88	10.8	181	2	Q6F0J1 MESFL
41	88	10.8	4705	1	FAT2 DROME
42	86.5	10.7	376	2	Q8K4E6 MOUSE
43	86.5	10.7	376	2	Q8K4E7 MOUSE
44	86.5	10.7	1037	2	Q4N4R1 THEPA
45	85.5	10.5	867	2	Q7RNN8 PLAYO
46	85	10.5	252	2	Q8JZN4 MOUSE
47	85	10.5	381	1	SPP2 SCHPO
48	84.5	10.4	376	2	Q8K4E8 MOUSE
49	84.5	10.4	443	2	Q5AVG0 EMENI
50	84	10.3	1101	2	Q6CIC3 KLULA
51	83.5	10.3	454	2	Q8HZU5 9CHIR
52	83.5	10.3	454	2	Q8HZU6 9CHIR
53	83.5	10.3	454	2	Q8HZU7 9CHIR
54	83.5	10.3	859	2	Q55C96 DICDI
55	83	10.2	289	2	Q5ONCO ENTHI
56	83	10.2	376	2	Q8JZN0 MOUSE
57	83	10.2	654	2	Q59MA6 CANAL
58	83	10.2	664	2	Q4Z297 PLABE
59	83	10.2	748	2	Q6ZNI6 HUMAN
60	83	10.2	788	2	Q6ZMV3 HUMAN
61	82.5	10.2	268	1	IL1A LAMGL
62	82.5	10.2	319	2	Q4FLU1 PRICK
63	82.5	10.2	780	2	Q5E4J4 VIBFI
64	82	10.1	263	2	Q74316 SCHPO
65	82	10.1	1156	2	Q7RH07 PLAYO
66	82	10.1	1374	2	Q54MY6 DICDI
67	82	10.1	1534	2	Q8MPV7 CAEEL
68	81.5	10.0	270	1	IL1A PIG
69	81.5	10.0	599	2	Q8I2G6 PLAF7
70	81.5	10.0	617	2	Q25986 PLAF7
71	81.5	10.0	1049	2	Q93KF0 9FIRM
72	81	10.0	264	2	Q5HD69 STAAC
73	81	10.0	267	1	IL1A RABIT
74	81	10.0	1085	2	Q6BMT0 DEBHA
75	80.5	9.9	825	2	Q8IC17 PLAF7
76	80.5	9.9	866	2	Q84500 CHLTR
77	80	9.9	1449	1	DPO3 CLOPE
78	80	9.9	1868	2	Q6BNV2 DEBHA
79	79.5	9.8	247	2	Q61OH0 CAEBR
80	79.5	9.8	522	2	Q5U508 XENLA
81	79.5	9.8	595	2	Q9SDM4 DUNTE
82	79.5	9.8	664	1	DNAK CHLCV
83	79.5	9.8	1044	2	Q94173 PNECA
84	79	9.7	425	2	Q4Z7S9 PLABE
85	79	9.7	452	1	PCBA HELPY
86	79	9.7	925	2	Q4YV66 PLABE
87	79	9.7	1017	2	Q54AZ4 DICDI
88	79	9.7	10578	2	Q8ISF5 CAEEL
89	79	9.7	18519	2	Q8ISF6 CAEEL
90	79	9.7	18534	2	Q8ISF7 CAEEL
91	78.5	9.7	204	2	Q9ZNI7 CLOHI
92	78.5	9.7	396	2	Q5XVE2 ARATH
93	78.5	9.7	420	2	Q5AGB9 CANAL
94	78.5	9.7	570	2	Q5CJX1 CRYHO
95	78.5	9.7	578	2	Q5CWL8 CRYPV
96	78.5	9.7	731	2	Q4YVY1 PLABE
97	78.5	9.7	1061	2	Q8DU02 STRMU
98	78.5	9.7	1518	2	Q512B0 ENTHI
99	78	9.6	261	2	Q7NAD8 MYCGA
100	78	9.6	261	2	Q8CU21 STAEP

ALIGNMENTS

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RESULT 1
ID Q6WJ7 HUMAN PRELIMINARY; PRT; 189 AA.
AC Q6WJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DELTA3PRO-IL-18.
GN Name=IL18;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaggero A., De Ambrosis A., Mezzanzanica D., Piazza T., Rubartelli A.,
RA Figini M., Canevari S., Ferrini S.;
RT "A novel isoform of pro-interleukin-18 expressed in ovarian tumors is
RT resistant to caspase-1 and -4 processing.";
RL Ensembl: AY266351; AARP2112.1; -; mRNA.
DR EMBL; Q6WJ7; 33-189.
DR SMR; Q6WJ7; 33-189.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SQR; Q6WJ7; 33-189.
SQ SEQUENCE 189 AA; 21896 MW; A8BA275CF713A4B6 CRC64;

Query Match 99.9%; Score 811; DB 2; Length 189;
Best Local Similarity 99.4%; Pred. No. 3.9e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIIFSIYKDSQPRGM 60
DB 33 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIIFSIYKDSQPRGM 92
QY 61 AVTISVCKEIKSLXSCENKIISFKEMPPDNKIDKSDIIFQFQSVPGHDKMKQFESSY 120
DB 93 AVTISVCKEIKSLXSCENKIISFKEMPPDNKIDKSDIIFQFQSVPGHDKMKQFESSY 152
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
DB 153 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 189

RESULT 2
IL18 HUMAN
ID IL18 HUMAN STANDARD; PRT; 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF, IL1F4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (MRNA).
RA Tissot-Livier;
RC MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.,
RA "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein.";
RL J. Immunol. 156:4274-4279 (1996).
RN [2]
RP NUCLEOTIDE SEQUENCE (MRNA).

```

Yong D., Guixin D., Lihua H., Haitao W.;  
 "Cloning and sequencing of the cDNA for precursor hIL-18.";  
 Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 [3]  
 NUCLEOTIDE SEQUENCE (MRNA).  
 Liu J., Peng X., Yuan J., Qiang B.;  
 "Cloning of human interleukin 18 cDNA.";  
 Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 [4]  
 NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).  
 TISSUE=Urinary bladder;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [5]  
 NUCLEOTIDE SEQUENCE OF 2-193.  
 TISSUE=Periphereal blood;  
 Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;  
 Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
 CC and stimulates interferon gamma production in T helper type I  
 CC cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; D49950; BAA08706.1; -; mRNA.  
 CC EMBL; AF077611; AAC27787.1; -; mRNA.  
 CC EMBL; AY044641; AAK95950.1; -; mRNA.  
 CC EMBL; BC007007; AAH07007.1; -; mRNA.  
 CC EMBL; BC007461; AAH07461.1; -; mRNA.  
 CC EMBL; U90434; AAB50010.1; -; mRNA.  
 CC PDB; 1JOS; NMR; A=37-193.  
 CC OGP; Q14116; -;  
 CC Ensembl; ENSG00000150782; Homo sapiens.  
 CC HGNC; HGNC:5986; IL18.  
 CC H-InvDB; HIX0010123; -;  
 CC MIM; 600953; -;  
 CC GO; GO:0005576; C:extracellular region; TAS.  
 CC GO; GO:0005125; F:cytokine activity; TAS.  
 CC GO; GO:0004871; F:signal transducer activity; TAS.  
 CC GO; GO:0001525; P:angiogenesis; IDA.  
 CC GO; GO:0007267; P:cell-cell signaling; TAS.  
 CC GO; GO:0042033; P:chemokine biosynthesis; TAS.  
 CC GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. . .; TAS.  
 CC GO; GO:0006955; P:immune response; TAS.  
 CC GO; GO:0042095; P:induction of apoptosis via death domain rec. . .; ISS.  
 CC GO; GO:0006625; P:induction of interferon-gamma biosynthesis; TAS.  
 CC GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.  
 CC GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.

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DR GO: 0042104; P: positive regulation of activated T cell pro. . . ; IDA.
DR GO: 0030155; P: regulation of cell adhesion; IDA.
DR GO: 0030431; P: sleep; ISS.
DR GO: 0042092; P: T-helper 2 type immune response; TAS.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW 3D-structure; Cytokine.
FT PROPEP 1 36
FT CHAIN 37 193
FT CONFLICT 66 66
FT CONFLICT 86 86
FT CONFLICT 86 86
FT CONFLICT 191 191
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.9%; Score 811; DB 1; Length 193;
Best Local Similarity 99.4%; Pred. No. 4e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 3
Q6FGY3_HUMAN
ID Q6FGY3_HUMAN PRELIMINARY; PRT; 193 AA.
AC Q6FGY3;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE IL18 protein.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schattner R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541973; CAG46771.1; -; mRNA.
DR EMBL; CR542001; CAG46798.1; -; mRNA.
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.9%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 4e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
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RESULT 4
Q96KJ8_HUMAN
ID Q96KJ8_HUMAN PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ying P., Jianxin L.,
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR SMR; Q96KJ8; 37-193.
DR GO: 0005576; C: extracellular region; IEA.
DR GO: 0005149; F: interleukin-1 receptor binding; IEA.
DR GO: 0006955; P: immune response; IEA.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.3%; Score 798; DB 2; Length 193;
Best Local Similarity 97.5%; Pred. No. 6.7e-67;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKDTSKDIIFQFQSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 5
Q9BG15_MACMU
ID Q9BG15_MACMU PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin-18.
GN Name=IL18;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21229850; PubMed=11331040; DOI=10.1089/107999001750133212;
RA Glavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the interleukin-18 gene from rhesus macaque by the
RT simian immunodeficiency virus does not result in increased viral
RT replication.";
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR SMR; Q9BG15; 37-193.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
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SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;
Query Match 97.5%; Score 792; DB 2; Length 193;
Best Local Similarity 95.5%; Pred. No. 2.5e-66;
Matches 150; Conservative .5; Mismatches 2; Indels 0; Gaps 0;

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DB 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 120
DB 97 AVAISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 6
IL18_HORSE
ID AC Q9XSO7; STANDARD; PRT; 193 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Argyle D.J., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Nicolson L., Onions D.E.;
RA "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Y11131; CAA72013.1; -; mRNA.
CC SMR; Q9XSO7; 37-193.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC Cytokine.
FT PROPEP 1 36 By similarity.
FT CHAIN 37 193 Interleukin-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 81.2%; Score 659; DB 1; Length 193;
Best Local Similarity 77.7%; Pred. No. 7.9e-54;
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
DB 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
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SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;
Query Match 81.2%; Score 659; DB 2; Length 193;
Best Local Similarity 77.7%; Pred. No. 7.9e-54;
Matches 122; Conservative 22; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 7
Q6TLW4_BUBBU
ID AC Q6TLW4_BUBBU PRELIMINARY; PRT; 193 AA.
DT 03-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Interleukin 18.
GN Name=IL18;
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chaudhury P., Bera B.C.;
RA "Cloning and sequencing of Indian water buffalo interleukin-18 cDNA.";
RA Bur. J. Immunogenet. 32:75-78(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chaudhuri P., Bera B.C.;
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AX394479; AAQ94552.1; -; mRNA.
DR SMR; Q6TLW4; 37-193.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SF; SF00340.1; IL1; 1.
SQ SEQUENCE 193 AA; 22176 MW; 66116F198DE94BC4 CRC64;

Query Match 81.2%; Score 659; DB 2; Length 193;
Best Local Similarity 77.7%; Pred. No. 7.9e-54;
Matches 122; Conservative 22; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFILSMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 KGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 8
Q6T573_BUBBU
ID AC Q6T573_BUBBU PRELIMINARY; PRT; 193 AA.
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Interleukin-18.
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Premraj A., Sreekumar E., Rasool T.J.;
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436506; AAR29081.1; -; mRNA.
DR SMR; Q6T573; 37-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
```

```
DR Pfam; PF00340; IL1; 1.
SQ SEQUENCE 193 AA; 22190 MW; 93103E5C62B745DE CRC64;

Query Match      81.2%; Score 659; DB 2; Length 193;
Best Local Similarity 77.1%; Pred. No. 7.9e-54;
Matches 122; Conservative 22; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIIISMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCDNDNAPQTIFIIIMYKDSLTRL 96

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQSVPGHDKNMQFESSY 120
DB 97 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSDIIFQSVPGHDDKIQFESSLY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 KGYFLACKENDLFLKILKQDDNGDKSYMFTVQNGN 193
```

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RESULT 9
Q9MZL8_BOVIN PRELIMINARY; PRT; 178 AA.
ID Q9MZL8_BOVIN
AC Q9MZL8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DR 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OS Interleukin-18 (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrl M., Bolin C.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -; mRNA.
DR HSP; Q14116; IJ05.
DR SMR; Q9MZL8; 22-178.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:000149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR NON_TER 178 178
FT NON_TER
SQ SEQUENCE 178 AA; 20631 MW; 815D6B2B88ACB497 CRC64;

Query Match      80.5%; Score 654; DB 2; Length 178;
Best Local Similarity 77.1%; Pred. No. 2.1e-53;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIIISMYKDSQPRGM 60
DB 22 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCDNDNAPQTIFIIIMYKDSLTRL 81

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQSVPGHDKNMQFESSY 120
DB 82 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSDIIFQSVPGHDDKIQFESSLY 141

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 142 KGYFLACKENDLFLKILKQDDNDRKSYMFTVQNGN 178
```

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RESULT 10
IL18_BOVIN
ID IL18_BOVIN
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
```

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20012648; PubMed=10547157; DOI=10.1089/1079990999313118;
RA Shoda L.K., Zarling D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity."
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC !- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type 1
CC cells (By similarity).
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- SIMILARITY: Belongs to the IL-1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF124789; AAF08686.1; -; mRNA.
DR SMR; Q9TU73; 37-193.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR Cytokine.
KW PROPEP 1 36 By similarity.
FT CHAIN 37 193 Interleukin-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match      80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 2.3e-53;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIIISMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCDNDNAPQTIFIIIMYKDSLTRL 96

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQSVPGHDKNMQFESSY 120
DB 97 AVTISVQCKMSTLSCENKIVSFKEMNPPDNIDNEGSDIIFQSVPGHDDKIQFESSLY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 KGYFLACKENDLFLKILKQDDNDRKSYMFTVQNGN 193

RESULT 11
Q5I931_BOSTR PRELIMINARY; PRT; 193 AA.
ID Q5I931_BOSTR
AC Q5I931;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Interleukin-18.
OS Boselaphus tragocamelus (Nilgai).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Boselaphus.
OX NCBI_TaxID=9917;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Saini M., Swarup D., Yadav M.P., Singh G.R., Arora B.M., Chandra P.,
RA Das D.K., Gupta P.K.;
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RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY842499; AAW34191.1; -, mRNA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
SQ SEQUENCE 193 AA; 22130 MW; 75B6671696EB4A8D CRC64;

Query Match 80.2%; Score 651; DB 2; Length 193;
Best Local Similarity 77.6%; Pred. No. 4.5e-53;
Matches 121; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 HFGKLEPKLSIIRNLNDQVLFINGNQPVFEDMPDSCPNAPQTIIFIYWKDSLTRL 96
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 AVTISVQCKMSTLSCENKIISFKEMNPPDNIDEGSDIIFQFQSVPGHDKMKQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 156
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 KGFLACKENDLFKLILKQDDNGDKSVTFVQNQ 192

RESULT 12
Q9GL09_SHEEP PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-18 (IGIF).
GN Names=11-18;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401033; CAC09326.2; -, mRNA.
DR HSP; Q14116; 1J08.
DR SMR; Q9GL09; 37-193.
DR GO; GO:0005776; C:extracellular region; IEA.
DR GO; GO:0005149; F:Interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 79.8%; Score 648; DB 2; Length 193;
Best Local Similarity 77.7%; Pred. No. 8.5e-53;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 HFGKLEPKLSIIRNLNDQVLFISQGNQPVFEDMPDSCDNAPQTIIFIYWKDSLTRL 96
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 AVTISVQCKMSTLSCENKIISFKEMNPPDNIDEGSDIIFQFQSVPGHDKMKQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 KGFLACKENDLFKLILKQDDNRDKSIMFTVQNK 193

RESULT 13
Q6QVC4_CAPHI PRELIMINARY; PRT; 159 AA.
ID Q6QVC4_CAPHI
AC Q6QVC4;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-18 (Fragment).
GN Names=11-18;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RA Liu W., Sul Z., Zhao H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY524275; AAS13327.1; -, mRNA.
DR SMR; Q6QVC4; 3-159.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 159 AA; 18331 MW; FDCDEAAF15278FFC CRC64;

Query Match 79.7%; Score 647; DB 2; Length 159;
Best Local Similarity 77.1%; Pred. No. 8.4e-53;
Matches 121; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 HFGKLEPKLSIIRNLNDQVLFISQGNQPVFEDMPDSCDNAPQTIIFIYWKDSLTRL 62
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNKDTKSDIIFQFQSVPGHDKMKQFESSY 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 AVTISVQCKMSTLSCENKIISFKEMNPPDNIDEGSDIIFQFQSVPGHDKMKQFESSLY 122
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 KGFLACKENDLFKLILKQDDNRDKSIMFTVQNK 159

RESULT 14
IL18_PIG STANDARD; PRT; 192 AA.
AC Q19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor).
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX NCBI_TaxID=9823;
RN [1]
RA Foss D.L., Murtough M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DE [2]
DE NUCLEOTIDE SEQUENCE.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DE [3]
DE NUCLEOTIDE SEQUENCE.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DE [4]
DE NUCLEOTIDE SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849; DOI=10.1007/s002510050630;
RA Fournout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RA "Cloning, chromosomal location, and tissue expression of the gene for
```



RT pig interleukin-18.";  
 RL Immunogenetics 51:358-365(2000).  
 CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
 CC and stimulates interferon gamma production in T helper type I  
 CC cells (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC -----  
 DR EMBL; U68701; AAC18415.1; -; mRNA.  
 DR EMBL; Y11132; CAA72014.1; -; mRNA.  
 DR EMBL; AB010003; BAA24135.1; -; mRNA.  
 DR EMBL; AF191088; AAF71200.1; -; mRNA.  
 DR SMR; O19073; 36-192.  
 DR GO; GO:0005576; C:extracellular region; ISS.  
 DR GO; GO:0005125; F:cytokine activity; IMP.  
 DR GO; GO:0001525; P:angiogenesis; ISS.  
 DR GO; GO:0042033; P:chemokine biosynthesis; ISS.  
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.  
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.  
 DR GO; GO:0042104; P:positive regulation of activated T cell pro. .; ISS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR SMART; SM00125; IL1; 1.  
 KW Cytokine.  
 FT PROPEP 1 35 By similarity.  
 FT CHAIN 36 192 Interleukin-18.  
 SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;  
 Best Local Similarity 75.2%; Pred. No. 9.2e-52;  
 Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCRDNAPRTIFITISMYKDSQPRGM 60  
 DB 36 YFGKLEPKLSIIRNLNDQVLFINGHQAVFEDPDSDCSDNAPQTVFIYMYKDSLTRL 95  
 QY 61 AVTISVCKEKSIXLSCENKIISFKEMNPPDNIKTKSDIIFQSVPGHDKMOPFESSY 120  
 DB 96 AVTISVCKKASTLSCKNKTLSFKEMSPDNIDDEGNDIIFQSVPGHDDKIQFESSLY 155  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 156 KGYFLACKENDLFLKILKKEDECGDKSIMFTVQKN 192

RESULT 15  
 Q95M33\_FELCA  
 ID Q95M33\_FELCA PRELIMINARY; PRT; 192 AA.  
 AC Q95M33;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)  
 DE Interferon-gamma inducing factor (IL-18).  
 GN Name=IGIF;  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
 OC Felis.  
 OC NCBI\_TaxID=9685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Qiao J., Xia X., Yang S.;

RT "Cloning and sequence analysis of feline IL-18 gene.";  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y13923; CAC42918.1; -; mRNA.  
 DR EMBL; DQ100372; AAY96319.1; -; mRNA.  
 DR HSSP; Q14116; LJOS.  
 DR SMR; Q95M33; 36-192.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 78.1%; Score 634; DB 2; Length 192;  
 Best Local Similarity 76.4%; Pred. No. 1.8e-51;  
 Matches 120; Conservative 21; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSCRDNAPRTIFITISMYKDSQPRGM 60  
 DB 36 YFGKLEHKLISIRNLNDQVLFINGDQVFEFDPDSCTDNAPRTFIIYMYKDSLTRL 95  
 QY 61 AVTISVCKEKSIXLSCENKIISFKEMNPPDNIKTKSDIIFQSVPGHDKMOPFESSY 120  
 DB 96 AVTISVNYKTMSTLSCENKIISFKEMSPDESINDEGNDIIFQSVPGHDDKIQFESSLY 155  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 156 KGYFLACEKEKDLFKLILKKEDEGDKSIMFTVQKN 192

Search completed: January 30, 2006, 08:40:13  
 Job time : 166 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:41:09 ; Search time 31 Seconds

(without alignments)

54.844 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

1: /cgm2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgm2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgm2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgm2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*  
7: /cgm2\_6/ptodata/1/pubpaa/US12\_NEW\_PUB pep.\*  
8: /cgm2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	6	US-10-401-386B-64
2	805	99.1	157	6	US-10-401-386B-76
3	803	98.9	157	6	US-10-401-386B-78
4	799	98.4	157	6	US-10-401-386B-70
5	798	98.3	157	6	US-10-401-386B-66
6	798	98.3	157	6	US-10-401-386B-80
7	795	97.9	157	6	US-10-401-386B-68
8	792	97.5	157	6	US-10-401-386B-72
9	86.5	10.7	376	7	US-11-012-762-22
10	86.5	10.7	376	7	US-11-012-762-24
11	85	10.5	252	7	US-11-012-762-14
12	84.5	10.4	376	7	US-11-012-762-20
13	83	10.2	376	7	US-11-012-762-10
14	83	10.2	376	7	US-11-012-762-16
15	83	10.2	376	7	US-11-012-762-40
16	74.5	9.2	376	7	US-11-012-762-18
17	74.5	9.2	467	7	US-11-127-817-15
18	74	9.1	261	6	US-10-793-626-584
19	74	9.1	261	6	US-10-793-626-982
20	70	8.6	2668	7	US-11-124-368A-214
21	70	8.6	2668	7	US-11-124-368A-215
22	66.5	8.2	614	7	US-11-150-845-34
23	64.5	7.9	414	6	US-10-631-558-2
24	64	7.9	619	6	US-10-517-939-352
25	63.5	7.8	479	6	US-10-517-939-350

Sequence 397, App  
Sequence 3298, App  
Sequence 776, App  
Sequence 672, App  
Sequence 46, Appli  
Sequence 1, Appli  
Sequence 84, Appli  
Sequence 557, App  
Sequence 3218, App  
Sequence 330, App  
Sequence 14, Appli  
Sequence 1056, App  
Sequence 6, Appli  
Sequence 20, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 1121, App  
Sequence 1134, App  
Sequence 1136, App  
Sequence 1142, App  
Sequence 1132, App  
Sequence 12, Appli  
Sequence 3, Appli  
Sequence 171, App  
Sequence 187, App  
Sequence 31, Appli  
Sequence 572, App  
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Sequence 578, App  
Sequence 568, App  
Sequence 82, Appli  
Sequence 570, App  
Sequence 28, Appli  
Sequence 580, App  
Sequence 600, App  
Sequence 594, App  
Sequence 5, Appli  
Sequence 586, App  
Sequence 592, App  
Sequence 602, App  
Sequence 2, Appli  
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Sequence 1648, App  
Sequence 2364, App  
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Sequence 1478, App  
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Sequence 52, Appli  
Sequence 145, App  
Sequence 144, App  
Sequence 24, Appli  
Sequence 533, App  
Sequence 3256, App  
Sequence 68, Appli  
Sequence 130, App  
Sequence 154, App  
Sequence 262, App  
Sequence 1436, App  
Sequence 36, Appli  
Sequence 43, Appli  
Sequence 111, App  
Sequence 51, App  
Sequence 195, App  
Sequence 9, Appli  
Sequence 1059, App  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 933, App  
Sequence 5, Appli  
Sequence 119, App  
Sequence 8, Appli  
Sequence 11, Appli



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; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-70

Query Match 98.4%; Score 799; DB 6; Length 157;
Best Local Similarity 98.1%; Pred. No. 4.4e-79;
Matches 154; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6
US-10-401-386B-80
; Sequence 80, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-80

Query Match 98.3%; Score 798; DB 6; Length 157;
Best Local Similarity 97.5%; Pred. No. 5.6e-79;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVAISVKCEKISTLSKSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
US-10-401-386B-68
; Sequence 68, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; Sequence 66, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-66

Query Match 98.3%; Score 798; DB 6; Length 157;
Best Local Similarity 97.5%; Pred. No. 5.6e-79;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISTLSKSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
US-10-401-386B-66
; Sequence 66, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-66

Query Match 98.3%; Score 798; DB 6; Length 157;
Best Local Similarity 97.5%; Pred. No. 5.6e-79;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Db 112 GVKFEVQSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLKPNQOQFYANLI 170
Qy 104 --RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDELGD 146
Db 171 SGRTPPGKEGKLSICFMGLRKYFLNCRPTKLRLLRLVTHWYQLCKE-KLGD 221

RESULT 11
US-11-012-762-14
; Sequence 14, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-14

Query Match 10.5%; Score 85; DB 7; Length 252;
Best Local Similarity 23.1%; Pred. No. 0.045; Indels 66; Gaps 8;
Matches 42; Conservative 25; Mismatches 49;

Qy 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKD 54
Db 68 GRSDADLVFLNLTSPEDQLNQGVLIKEIKQLCEVQHERRC----- 111

Qy 55 SOPRGMATISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTKSDII----- 100
Db 112 -----GVKFEVHLSRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLK 160
Qy 101 ----FFQ-----RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db 161 PNQOQFYANLISGRTPPGKEGKLSICFMGLQKYFLNCRPTKLRLLRLVTHWYQLCKE-KL 219

Qy 145 GD 146
Db 220 GD 221

RESULT 12
US-11-012-762-20
; Sequence 20, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-20

Query Match 10.4%; Score 84.5; DB 7; Length 376;
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Best Local Similarity 23.3%; Pred. No. 0.086;
Matches 40; Conservative 28; Mismatches 65; Indels 39; Gaps 7;

Qy 5 LESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMATVI 64
Db 59 VKGCKTALKGRSDADLVFLNLTSPEDQLNQ-----QGVLIKEIKQLVEVQHERRF 111

Qy 65 SVKCEKISXLSKSCENKIISFKEMNPPDNIKDTKSDII-----FFQ---- 103
Db 112 GVKFEVQSLRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLKPNQOQFYANLI 170
Qy 104 --RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDELGD 146
Db 171 SGRTPPGKEGKLLICFMGLRKYFLNCRPTKLRLLRLVTHWYQLCKE-KLGD 221

RESULT 13
US-11-012-762-10
; Sequence 10, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-10

Query Match 10.2%; Score 83; DB 7; Length 376;
Best Local Similarity 23.1%; Pred. No. 0.12;
Matches 42; Conservative 24; Mismatches 50; Indels 66; Gaps 8;

Qy 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKD 54
Db 68 GRSDADLVFLNLTSPEDQLNQGVLIKEIKQLCEVQHERRC----- 111

Qy 55 SOPRGMATISVKCEKISXLSKSCENKIISFKEMNPPDNIKDTKSDII----- 100
Db 112 -----GVKFEVHLSRSPNSRALSFK-LSAPDLLKEVKFDVLPAYDLDLHLNLLK 160
Qy 101 ----FFQ-----RSVPGHDKNQMFSSSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db 161 PNQOQFYANLISGRTPPGKEGKLSICFMGLRKYFLNCRPTKLRLLRLVTHWYQLCKE-KL 219

Qy 145 GD 146
Db 220 GD 221

RESULT 14
US-11-012-762-16
; Sequence 16, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
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Job time : 32 secs

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; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-16

Query Match      10.2%; Score 83; DB 7; Length 376;
Best Local Similarity 23.1%; Pred. No. 0.12;
Matches 42; Conservative 24; Mismatches 50; Indels 66; Gaps 8;

Qy      3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMVKD 54
Db      68 GRSDADLVVFLNNITSFEDQLNQOGLVLIKEIKKQLCEVQHERRC-----111

Qy      55 SQPRGMATVISVCKEKISXLSCEKNIISFKEMNPPDNIKOTKSDII-----100
Db      112 -----GVKFEVHSLRSPNSRAISFK-LSAPDLLKEVKFDVLPAYDLLDHLNLIK 160

Qy      101 -----FFQ-----RSVPGHNDNMQFESSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db      161 PNOQFYANLISGRTPPGKEGKLSICFMGLRKYFLNCRPTKLRLIRLVTHWYQLCKE-KL 219

Qy      145 GD 146
Db      220 GD 221

RESULT 15
US-11-012-762-40
; Sequence 40, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-40

Query Match      10.2%; Score 83; DB 7; Length 376;
Best Local Similarity 23.1%; Pred. No. 0.12;
Matches 42; Conservative 24; Mismatches 50; Indels 66; Gaps 8;

Qy      3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCDNAPRTIFIISMVKD 54
Db      68 GRSDADLVVFLNNITSFEDQLNQOGLVLIKEIKKQLCEVQHERRC-----111

Qy      55 SQPRGMATVISVCKEKISXLSCEKNIISFKEMNPPDNIKOTKSDII-----100
Db      112 -----GVKFEVHSLRSPNSRAISFK-LSAPDLLKEVKFDVLPAYDLLDHLNLIK 160

Qy      101 -----FFQ-----RSVPGHNDNMQFESSYEGYFLACE--KERDLFKLI-----LKKEDEL 144
Db      161 PNOQFYANLISGRTPPGKEGKLSICFMGLRKYFLNCRPTKLRLIRLVTHWYQLCKE-KL 219

Qy      145 GD 146
Db      220 GD 221

Search completed: January 30, 2006, 08:52:39
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:40:23 ; Search time 117 Seconds

(without alignments)  
560.677 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESLKSVIRNLNDQVL.....LKKEDELGDRSINFVQNE 157

Scoring table: BLOSUM62

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:\*

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*

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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	3	US-09-775-046-9 Sequence 9, Appli
2	811	99.9	157	3	US-09-030-061-6 Sequence 6, Appli
3	811	99.9	157	4	US-10-100-057-6 Sequence 6, Appli
4	811	99.9	157	4	US-10-094-153-2 Sequence 2, Appli
5	811	99.9	157	4	US-10-260-576-4 Sequence 4, Appli
6	811	99.9	157	4	US-10-297-136-1 Sequence 1, Appli
7	811	99.9	157	4	US-10-311-491-3 Sequence 3, Appli
8	811	99.9	157	4	US-10-397-786A-3 Sequence 3, Appli
9	811	99.9	157	4	US-10-280-609-1 Sequence 1, Appli
10	811	99.9	157	4	US-10-646-308-14 Sequence 14, Appli
11	811	99.9	157	5	US-10-872-198-98 Sequence 98, Appli
12	811	99.9	157	5	US-10-823-964A-1 Sequence 1, Appli
13	811	99.9	157	5	US-10-666-490A-1 Sequence 1, Appli
14	811	99.9	157	5	US-10-518-333-1 Sequence 1, Appli
15	811	99.9	157	6	US-11-021-951-98 Sequence 98, Appli
16	811	99.9	158	4	US-10-693-195-7 Sequence 7, Appli
17	811	99.9	158	4	US-10-694-978-7 Sequence 7, Appli
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25	811	99.9	233	4	US-10-311-491-10 Sequence 10, Appli
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27	811	99.9	361	5	US-10-895-396-8 Sequence 8, Appli

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29	810	99.8	157	3	US-09-752-510-6 Sequence 6, Appli
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31	810	99.8	157	4	US-10-327-069-1 Sequence 1, Appli
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34	810	99.8	193	4	US-10-646-308-13 Sequence 13, Appli
35	807	99.4	157	4	US-10-094-153-10 Sequence 10, Appli
36	807	99.4	193	4	US-10-094-153-9 Sequence 9, Appli
37	805	99.1	157	4	US-10-094-153-6 Sequence 6, Appli
38	805	99.1	157	4	US-10-094-153-7 Sequence 7, Appli
39	805	99.1	193	4	US-10-094-153-4 Sequence 4, Appli
40	805	99.1	193	4	US-10-094-153-3 Sequence 3, Appli
41	805	99.1	325	5	US-10-895-396-11 Sequence 11, Appli
42	805	99.1	361	5	US-10-895-396-9 Sequence 9, Appli
43	803	98.9	157	4	US-10-105-080-10 Sequence 10, Appli
44	803	98.9	193	4	US-10-105-080-4 Sequence 4, Appli
45	801	98.6	157	3	US-09-030-061-20 Sequence 20, Appli
46	801	98.6	157	4	US-10-100-057-20 Sequence 20, Appli
47	801	98.6	157	4	US-10-260-576-6 Sequence 6, Appli
48	801	98.6	157	5	US-10-823-964A-4 Sequence 4, Appli
49	799	98.4	193	4	US-10-094-153-8 Sequence 8, Appli
50	799	98.4	193	4	US-10-094-153-5 Sequence 5, Appli
51	795.5	98.0	156	4	US-10-414-774-1 Sequence 1, Appli
52	791	97.4	157	3	US-09-030-061-21 Sequence 21, Appli
53	791	97.4	157	3	US-09-030-061-22 Sequence 22, Appli
54	791	97.4	157	4	US-10-100-057-21 Sequence 21, Appli
55	791	97.4	157	4	US-10-100-057-22 Sequence 22, Appli
56	791	97.4	157	4	US-10-260-576-7 Sequence 7, Appli
57	791	97.4	157	4	US-10-260-576-8 Sequence 8, Appli
58	786	96.8	157	5	US-10-823-964A-9 Sequence 9, Appli
59	785	96.7	157	5	US-10-823-964A-10 Sequence 10, Appli
60	784	96.6	157	5	US-10-823-964A-7 Sequence 7, Appli
61	783	96.4	157	5	US-10-823-964A-8 Sequence 8, Appli
62	782	96.3	157	3	US-09-030-061-25 Sequence 25, Appli
63	782	96.3	157	4	US-10-100-057-25 Sequence 25, Appli
64	782	96.3	157	4	US-10-260-576-11 Sequence 11, Appli
65	781	96.2	157	3	US-09-030-061-23 Sequence 23, Appli
66	781	96.2	157	4	US-10-100-057-23 Sequence 23, Appli
67	781	96.2	157	4	US-10-260-576-9 Sequence 9, Appli
68	780	96.1	157	5	US-10-823-964A-5 Sequence 5, Appli
69	780	96.1	157	5	US-10-823-964A-6 Sequence 6, Appli
70	772	95.1	157	3	US-09-030-061-26 Sequence 26, Appli
71	772	95.1	157	4	US-10-100-057-26 Sequence 26, Appli
72	772	95.1	157	4	US-10-260-576-12 Sequence 12, Appli
73	771	95.0	157	3	US-09-030-061-24 Sequence 24, Appli
74	771	95.0	157	4	US-10-100-057-24 Sequence 24, Appli
75	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
76	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
77	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
78	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
79	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
80	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
81	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
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86	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
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88	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
89	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
90	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
91	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
92	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
93	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
94	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
95	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
96	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
97	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
98	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
99	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli
100	771	95.0	157	4	US-10-260-576-10 Sequence 10, Appli



## ALIGNMENTS

```
RESULT 1
US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-9

Query Match          99.9%; Score 811; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDNKNQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDNKNQFESSY 120
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 2
US-09-030-061-6
; Sequence 6, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDNKNQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDNKNQFESSY 120
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 3
US-10-100-057-6
; Sequence 6, Application US/10100057
; Publication No. US20020150555A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20020150555A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/100,057
; FILING DATE: 19-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
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; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-030-061-6
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Query Match          99.9%; Score 811; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDNKNQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGHDNKNQFESSY 120
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
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RESULT 3
US-10-100-057-6
; Sequence 6, Application US/10100057
; Publication No. US20020150555A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20020150555A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/100,057
; FILING DATE: 19-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4  
US-10-094-153-2  
; Sequence 2, Application US/10094153  
; Publication No. US20020169291A1  
; GENERAL INFORMATION:  
; APPLICANT: Dinarello, Charles  
; APPLICANT: Kim, Soo Hyun  
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use  
; FILE REFERENCE: 475  
; CURRENT APPLICATION NUMBER: US/10/094,153  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-094-153-2

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5  
US-10-260-576-4  
; Sequence 4, Application US/10260576  
; Publication No. US20030092130A1  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, Koza  
; APPLICANT: OKAMOTO, Iwao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 7th Street N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/260,576  
FILING DATE: 01-Oct-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/982,285  
FILING DATE: <Unknown>  
APPLICATION NUMBER: JP 333,037/96  
FILING DATE: No. US20030092130A1ember 29, 1996  
APPLICATION NUMBER: JP 20,906/97  
FILING DATE: January 21, 1997  
APPLICATION NUMBER: JP 10,053,503  
FILING DATE: No. US20030092130A1ember 14, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: YAMAMOTO=15  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-260-576-4

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVCKEIKSLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6  
US-10-297-136-1  
; Sequence 1, Application US/10297136  
; Publication No. US20030113292A1  
; GENERAL INFORMATION:  
; APPLICANT: ESSER, KLAUS M.  
; APPLICANT: ROSENBERG, MARTIN  
; APPLICANT: TAL-SINGER, RUTH  
; APPLICANT: WOODNUTT, GARY  
; APPLICANT: CHISARI, FRANCIS V.  
; APPLICANT: DILLON, SUSAN B.  
; TITLE OF INVENTION: Methods of Treating Viral Diseases with  
; FILE REFERENCE: P51144  
; CURRENT APPLICATION NUMBER: US/10/297,136  
; CURRENT FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: PCT/US01/17924

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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
US-10-311-491-3
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
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Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8
US-10-397-786A-3
; Sequence 3, Application US/10397786A
; Publication No. US20040018195A1
; GENERAL INFORMATION:
; APPLICANT: Griswold, Donald
; APPLICANT: Li, Li
; APPLICANT: Li, Jian
; TITLE OF INVENTION: DIABETES DISEASE DERIVED PROTEINS, COMPOSITIONS, METHODS AND USE
; FILE REFERENCE: CEN-0287
; CURRENT APPLICATION NUMBER: US/10/397,786A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,902
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-397-786A-3

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDKTSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-10-280-609-1
; Sequence 1, Application US/10280609
; Publication No. US2004002336A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George
; APPLICANT: Snyder, Linda Anne
; APPLICANT: McCarthy, Stephen G.
; TITLE OF INVENTION: IL-18 OR MUT-IL-18R PROTEINS, ANTIBODIES, COMPOSITIONS,
; FILE REFERENCE: CEN0321
; CURRENT APPLICATION NUMBER: US/10/280,609
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/335,880
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-609-1

Query Match          99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
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Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 10

US-10-646-308-14  
; Sequence 14, Application US/10646308  
; Publication No. US20040136992A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Paul B. J.  
; APPLICANT: DEISHER, Theresa A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 3432-B  
; CURRENT APPLICATION NUMBER: US/10/646,308  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: --to be assigned--  
; PRIOR FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: 60/406,418  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-646-308-14

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 11

US-10-872-198-98  
; Sequence 98, Application US/10872198  
; Publication No. US2005002897A1  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich HAUPTS  
; APPLICANT: Andre KOLTERMANN  
; APPLICANT: Andreas SCHERDIG  
; APPLICANT: Christian VOETSMERIER  
; APPLICANT: Ulrich Ketting  
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF  
; FILE REFERENCE: 04156.0002U4  
; CURRENT APPLICATION NUMBER: US/10/872,198  
; CURRENT FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 60/543,518  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/524,960  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: EP 04003058  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: EP 03025871  
; PRIOR FILING DATE: 2003-11-11  
; PRIOR APPLICATION NUMBER: EP 03025851  
; PRIOR FILING DATE: 2003-11-10

; PRIOR APPLICATION NUMBER: EP 03013819  
; PRIOR FILING DATE: 2003-06-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 98  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-872-198-98

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 12

US-10-823-964A-1  
; Sequence 1, Application US/10823964A  
; Publication No. US20050008615A1  
; GENERAL INFORMATION:  
; APPLICANT: BAM, NARENDRA  
; APPLICANT: BONGERS, JACOB  
; APPLICANT: KIRKPATRICK, ROBERT B.  
; APPLICANT: JONSON, CHERYL A.  
; APPLICANT: JOHANSON, KYUNG  
; APPLICANT: QIU, XIANYANG  
; APPLICANT: YEH, PING  
; TITLE OF INVENTION: CONJUGATES COMPRISING HUMAN IL-18 AND  
; FILE REFERENCE: PU60053  
; CURRENT APPLICATION NUMBER: US/10/823,964A  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: 60/462,947  
; PRIOR FILING DATE: 2003-04-15  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-823-964A-1

Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 2.3e-78;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKOTKSDIIFQSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
RESULT 13  
US-10-666-490A-1

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; Sequence 1, Application US/10666490A
; Publication No. US20050063944A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jian;
; APPLICANT: Mbow, Lamine;
; APPLICANT: Goletz, Terry;
; APPLICANT: Peritt, David;
; TITLE OF INVENTION: METHOD OF INDUCING MATURATION OF DENDRITIC CELLS AND USES THEREOF
; FILE REFERENCE: CEN0312 NP
; CURRENT APPLICATION NUMBER: US/10/666,490A
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: 60/412,145
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver 3.0.
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-490A-1

Query Match          99.9%; Score 811; DB 5; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 14
US-10-518-333-1
; Sequence 1, Application US/10518333
; Publication No. US20050153880A1
; GENERAL INFORMATION:
; APPLICANT: Goto, Yukio
; APPLICANT: Kikkawa, Hideo
; APPLICANT: Kinoshita, Mine
; TITLE OF INVENTION: Method of Treating or Preventing IBD
; TITLE OF INVENTION: with IL-18
; FILE REFERENCE: TB00005
; CURRENT APPLICATION NUMBER: US/10/518,333
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/EP03/17744
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/392,176
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-518-333-1

Query Match          99.9%; Score 811; DB 5; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMVKDSQPRGM 60
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QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQSVPGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 15
US-11-021-951-98
; Sequence 98, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 98
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-98

Query Match          99.9%; Score 811; DB 6; Length 157;
Best Local Similarity 99.4%; Pred. No. 2.3e-78;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

Search completed: January 30, 2006, 08:51:56
Job time : 118 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:33:47 ; Search time 47 Seconds  
(without alignments)  
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Title: US-09-716-356A-6

Perfect score: 812

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	811	99.9	157	2	US-09-700-609-1
3	811	99.9	157	2	US-09-775-046-9
4	811	99.9	157	2	US-10-100-057-6
5	811	99.9	158	2	US-09-398-412B-7
6	811	99.9	164	2	US-09-949-016-10506
7	811	99.9	193	1	US-08-896-605A-6
8	810	99.8	157	1	US-08-896-605A-6
9	810	99.8	157	1	US-08-896-501A-4
10	810	99.8	157	2	US-08-884-324-1
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12	810	99.8	157	2	US-08-558-818-1
13	810	99.8	157	2	US-08-974-469A-1
14	810	99.8	157	2	US-08-832-180-1
15	810	99.8	157	2	US-08-832-198-6
16	810	99.8	157	2	US-09-819-902-6
17	810	99.8	157	2	US-09-752-510-6
18	810	99.8	157	2	US-09-711-899-1
19	810	99.8	157	2	US-09-556-972-26
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22	810	99.8	193	1	US-08-896-605A-2
23	810	99.8	193	1	US-08-896-501A-2
24	810	99.8	157	2	US-08-832-180-9
25	803	99.8	157	2	US-10-105-080-10
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27	801	98.6	157	2	US-08-982-285-6

28	801	98.6	157	2	US-10-100-057-20	Sequence 20, Appl
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30	791	97.4	157	2	US-08-982-285-7	Sequence 7, Appl
31	791	97.4	157	2	US-08-982-285-8	Sequence 8, Appl
32	791	97.4	157	2	US-10-100-057-21	Sequence 22, Appl
33	791	97.4	157	2	US-10-100-057-22	Sequence 21, Appl
34	782	96.3	157	2	US-08-982-285-11	Sequence 11, Appl
35	782	96.3	157	2	US-10-100-057-25	Sequence 25, Appl
36	781	96.2	157	2	US-08-982-285-9	Sequence 9, Appl
37	781	96.2	157	2	US-10-100-057-23	Sequence 12, Appl
38	772	95.1	157	2	US-08-982-285-12	Sequence 12, Appl
39	772	95.1	157	2	US-10-100-057-26	Sequence 26, Appl
40	771	95.0	157	2	US-08-982-285-10	Sequence 10, Appl
41	771	95.0	157	2	US-10-100-057-24	Sequence 24, Appl
42	634	78.1	157	2	US-03-917-265A-12	Sequence 12, Appl
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44	613	75.5	179	2	US-09-445-724B-14	Sequence 14, Appl
45	613	75.5	193	2	US-09-445-724B-2	Sequence 2, Appl
46	613	75.5	193	2	US-09-445-724B-6	Sequence 6, Appl
47	610	75.1	154	2	US-09-917-265A-5	Sequence 5, Appl
48	517	63.7	157	2	US-08-982-285-13	Sequence 13, Appl
49	517	63.7	157	2	US-10-100-057-27	Sequence 27, Appl
50	515	63.4	157	2	US-08-982-285-5	Sequence 5, Appl
51	515	63.4	157	2	US-09-700-609-2	Sequence 2, Appl
52	515	63.4	157	2	US-10-105-080-11	Sequence 11, Appl
53	515	63.4	157	2	US-09-775-046-8	Sequence 8, Appl
54	515	63.4	157	2	US-10-100-057-7	Sequence 7, Appl
55	513	63.4	158	2	US-09-398-412B-8	Sequence 8, Appl
56	513	63.2	157	1	US-08-502-535B-2	Sequence 2, Appl
57	513	63.2	157	1	US-08-908-005A-2	Sequence 2, Appl
58	513	63.2	157	2	US-08-996-338-27	Sequence 27, Appl
59	513	63.2	157	2	US-08-558-818-7	Sequence 7, Appl
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61	513	63.2	157	2	US-08-832-180-8	Sequence 8, Appl
62	513	63.2	157	2	US-08-832-198-11	Sequence 11, Appl
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66	513	63.2	157	2	US-09-752-510-11	Sequence 11, Appl
67	513	63.2	157	2	US-09-711-899-7	Sequence 7, Appl
68	513	63.2	157	2	US-09-556-972-27	Sequence 27, Appl
69	513	63.2	157	2	US-09-649-063-2	Sequence 2, Appl
70	511	62.9	192	2	US-10-105-080-5	Sequence 5, Appl
71	505	62.2	157	2	US-08-982-285-14	Sequence 14, Appl
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73	359	44.2	133	2	US-09-917-265A-2	Sequence 2, Appl
74	259	31.9	50	2	US-08-832-198-2	Sequence 2, Appl
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76	259	31.9	50	2	US-09-752-510-2	Sequence 2, Appl
77	96	11.8	25	2	US-08-558-818-4	Sequence 4, Appl
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79	96	11.8	25	2	US-08-832-180-4	Sequence 4, Appl
80	96	11.8	25	2	US-08-832-198-8	Sequence 8, Appl
81	96	11.8	25	2	US-09-819-902-8	Sequence 8, Appl
82	96	11.8	25	2	US-09-752-510-8	Sequence 8, Appl
83	96	11.8	25	2	US-09-711-899-4	Sequence 4, Appl
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86	90	11.1	17	2	US-09-752-510-5	Sequence 5, Appl
87	90	11.1	17	2	US-10-100-057-13	Sequence 13, Appl
88	85	10.5	333	2	US-09-270-767-31995	Sequence 31995, A
89	85	10.5	333	2	US-09-270-767-47212	Sequence 47212, A
90	83	10.2	697	2	US-09-270-767-47212	Sequence 26663, A
91	81	10.0	155	6	US-09-248-796A-26663	Patent No. 5494663
92	81	10.0	267	6	US-09-248-796A-19880	Patent No. 5494663
93	78.5	9.7	363	2	US-09-248-796A-20638	Sequence 19880, A
94	77	9.5	243	2	US-09-248-796A-20638	Sequence 20638, A
95	76.5	9.4	270	1	US-08-611-880-1	Sequence 1, Appl
96	76.5	9.4	270	2	US-09-085-305-13	Sequence 13, Appl
97	75.5	9.3	270	2	US-09-085-305-20	Sequence 20, Appl
98	75	9.2	267	2	US-09-134-001C-3520	Sequence 3520, Ap
99	75	9.2	637	2	US-09-248-796A-19134	Sequence 19134, A
100	74.5	9.2	467	2	US-09-522-775A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-982-285-4  
; Sequence 4, Application US/08982285  
; Patent No. 6476197  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, Kojo  
; APPLICANT: OKAMOTO, Iwao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 7th Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/982,285  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 333,037/96  
; FILING DATE: No. 6476197ember 29, 1996  
; APPLICATION NUMBER: JP 20,906/97  
; FILING DATE: January 21, 1997  
; APPLICATION NUMBER: JP 10,053,503  
; FILING DATE: No. 6476197ember 14, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-982-285-4

Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 2  
US-09-700-609-1  
; Sequence 1, Application US/09700609  
; Patent No. 6582689

; GENERAL INFORMATION:  
; APPLICANT: Johnson, Randall K  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: P50777  
; CURRENT APPLICATION NUMBER: US/09/700,609  
; CURRENT FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/086,560  
; PRIOR FILING DATE: 1999-05-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Human  
US-09-700-609-1  
Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 3  
US-09-775-046-9  
; Sequence 9, Application US/09775046  
; Patent No. 6843987  
; GENERAL INFORMATION:  
; APPLICANT: Debets, Johannes Eduard Maria Antonius  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS  
; FILE REFERENCE: DX01073K  
; CURRENT APPLICATION NUMBER: US/09/775,046  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/179,638  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-046-9

Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTSKDIIFFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 4

US-10-100-057-6  
; Sequence 6, Application US/10100057  
; Patent No. 6896880  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; HORMWOOD, Nicole Joy  
; UDAGAWA, No. 6896880yuyuki  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6

Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
  
QY 61 AVTISVKCEKISLSCENKIISFKENPPDNKOTKSDIIFQRSVPGHDNKKQFESSY 120  
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNKOTKSDIIFQRSVPGHDNKKQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

## RESULT 5

US-09-398-412B-7  
; Sequence 7, Application US/09398412B  
; Patent No. 6680380  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage  
; FILE REFERENCE: DX0904K

; CURRENT APPLICATION NUMBER: US/09/398,412B  
; CURRENT FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: US 60/100948  
; PRIOR FILING DATE: 1998-09-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-398-412B-7

Query Match 99.9%; Score 811; DB 2; Length 158;  
Best Local Similarity 99.4%; Pred. No. 4.7e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 61  
  
QY 61 AVTISVKCEKISLSCENKIISFKENPPDNKOTKSDIIFQRSVPGHDNKKQFESSY 120  
Db 62 AVTISVKCEKISLSCENKIISFKENPPDNKOTKSDIIFQRSVPGHDNKKQFESSY 121  
  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 122 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 158

## RESULT 6

US-09-949-016-10506  
; Sequence 10506, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10506  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-10506

Query Match 99.9%; Score 811; DB 2; Length 164;  
Best Local Similarity 99.4%; Pred. No. 5e-88;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 8 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 67  
  
QY 61 AVTISVKCEKISLSCENKIISFKENPPDNKOTKSDIIFQRSVPGHDNKKQFESSY 120  
Db 68 AVTISVKCEKISLSCENKIISFKENPPDNKOTKSDIIFQRSVPGHDNKKQFESSY 127  
  
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 128 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 164

## RESULT 7

US-09-949-016-6095



```
; Sequence 6095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6095
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6095

Query Match          99.9%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 6.2e-86;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 8
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 JULY 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618

; Sequence 6095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6095
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6095

Query Match          99.9%; Score 810; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKTKSDIIFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 9
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match          99.8%; Score 810; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 10
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takatori OKURA
; APPLICANT: Kakui TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: US/08/884,324
; CLASSIFICATION: 435
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1

Query Match          99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 11
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakui
; APPLICANT: OKURA, Takatori
; APPLICANT: KURIMOTO, Masahi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-338-26

Query Match          99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
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RESULT 12  
US-08-558-818-1  
; Sequence 1, Application US/08558818  
; Patent No. 6197297  
; GENERAL INFORMATION:  
; APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU  
; APPLICANT: KENKYUJO  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: FUKUDA, Shigeharu  
; APPLICANT: KURIMOTO, Masashi  
; APPLICANT: KOHNO, Keizo  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE  
; TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect Version 5.0  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: FELICI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/558,818  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: JP 58,240/95  
; PRIOR APPLICATION DATA: February 23, 1995  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-558-818-1

Query Match 99.8%; Score 810; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.2e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQPESSSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQPESSSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 13  
US-08-974-469A-1  
; Sequence 1, Application US/08974469A  
; Patent No. 6207641  
; GENERAL INFORMATION:

; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU  
; APPLICANT: KENKYUJO  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: FUKUDA, Shigeharu  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect Version 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,469A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/599,879  
; FILING DATE:  
; APPLICATION NUMBER: JP 78,357/95  
; FILING DATE: March 10, 1995  
; APPLICATION NUMBER: JP 274,988/95  
; FILING DATE: September 29, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-974-469A-1

Query Match 99.8%; Score 810; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.2e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQPESSSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQSVPGHDNKKQPESSSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 14  
US-08-832-180-1  
; Sequence 1, Application US/08832180  
; Patent No. 6214584  
; GENERAL INFORMATION:  
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU  
; APPLICANT: KENKYUJO  
; APPLICANT: USHIO, Shimpei  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: TANIMOTO, Tadao

APPLICANT: OKAMURA, Haruki  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING  
TITLE OF INVENTION: POLYPEPTIDE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/832,180  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/558,191  
FILING DATE:  
APPLICATION NUMBER: JP 304,203/94  
FILING DATE: No. 6214584ember 15, 1994  
APPLICATION NUMBER: 10048102  
FILING DATE: September 18, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: USHIO-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-832-180-1

Query Match 99.8%; Score 810; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.2e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 15  
US-08-832-198-6  
Sequence 6, Application US/08832198  
Patent No. 6242255  
GENERAL INFORMATION:  
APPLICANT: AKITA, Kenji  
APPLICANT: NUKADA, Yoshiyuki  
APPLICANT: FUJII, Mitsuhiro  
APPLICANT: TANIMOTO, Tadao  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA  
TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/832,198  
FILING DATE: 08-APR-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/721,018  
FILING DATE: 25-SEP-1996  
APPLICATION NUMBER: JP 95-270725  
FILING DATE: 26-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 96-067434  
FILING DATE: 29-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP not yet received  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: AKITA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" in position 73 is either  
OTHER INFORMATION: 'Ile' or 'Thr'  
US-08-832-198-6

Query Match 99.8%; Score 810; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.2e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCKENKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Search completed: January 30, 2006, 08:41:58  
Job time : 48 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: January 30, 2006, 08:19:16 ; Search time 134 Seconds  
(without alignments)  
514.795 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKLSVRLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A Geneseq 21:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	2	Aaw77077 Human int
2	811	99.9	157	3	Aay57570 Human int
3	811	99.9	157	4	Aag65351 Human int
4	811	99.9	157	4	Aag65294 Human int
5	811	99.9	157	4	Aae06661 Human int
6	811	99.9	157	5	Abb04389 Human IL-
7	811	99.9	157	5	Aae17134 Human IL-
8	811	99.9	157	5	Aae16954 Human act
9	811	99.9	157	6	Abg73359 Human wil
10	811	99.9	157	6	Ada50616 Human mat
11	811	99.9	157	6	Ada50610 Human mat
12	811	99.9	157	6	Abg83372 Human int
13	811	99.9	157	7	Ade06775 Human int
14	811	99.9	157	8	Ade54826 Human int
15	811	99.9	157	8	Adl24279 Human IL-
16	811	99.9	157	8	Adn35070 Human IL-
17	811	99.9	157	8	Adg73677 Human int
18	811	99.9	157	8	Adu06893 Human int
19	811	99.9	157	8	Adu49842 Human int
20	811	99.9	157	9	Adv900268 Protease-
21	811	99.9	157	9	Ady86605 Human rec
22	811	99.9	157	9	Adz77759 Human int
23	811	99.9	157	9	Adz77756 Human int
24	811	99.9	157	9	Aeb93714 Human mut

25	811	99.9	157	9	Aeb93702	Human wil
26	811	99.9	158	3	Aay85167	Human int
27	811	99.9	158	8	Adj88309	Human int
28	811	99.9	158	8	Ado04682	Human int
29	811	99.9	177	6	Ada50614	Mature co
30	811	99.9	180	2	Aaw48959	Wild-type
31	811	99.9	193	2	Aaw22047	Interfero
32	811	99.9	193	2	Aaw46592	Amino aci
33	811	99.9	193	4	Aab30541	A human I
34	811	99.9	193	4	Aag63830	Amino aci
35	811	99.9	193	5	Aae16953	Human pre
36	811	99.9	193	8	Adn41835	Amino aci
37	811	99.9	193	8	Adp12432	Protein e
38	811	99.9	193	8	Adp64786	Human int
39	811	99.9	193	9	Adz51271	Amino aci
40	811	99.9	193	9	Adz70835	Human int
41	811	99.9	193	9	Aeb28907	Human int
42	811	99.9	203	8	Adu06895	Human int
43	811	99.9	233	5	Aae16959	Ubiquitin
44	811	99.9	325	9	Ady22167	Human IL-
45	811	99.9	361	9	Ady22165	Human IL-
46	811	99.9	536	5	Aae16957	Human pro
47	811	99.9	588	5	Aae16958	Human pro
48	811	99.9	1048	5	Aae16960	Ubiquitin
49	810	99.8	157	2	Aar99564	Human int
50	810	99.8	157	2	Aar99558	Human mat
51	810	99.8	157	2	Aaw15701	Interfero
52	810	99.8	157	2	Aaw24258	Human pro
53	810	99.8	157	2	Aaw63810	Human IL-
54	810	99.8	157	2	Aaw52176	Interfero
55	810	99.8	157	2	Aaw77158	Human int
56	810	99.8	157	2	Aaw37741	IFN-gamma
57	810	99.8	157	2	Aay39799	Interleuk
58	810	99.8	157	3	Aay53904	Sequence
59	810	99.8	157	3	Aay44597	Human int
60	810	99.8	157	4	Aab82408	Human int
61	810	99.8	157	6	Abg83405	Human int
62	810	99.8	157	6	Abg83406	Human int
63	810	99.8	157	6	Abg83399	Human int
64	810	99.8	157	6	Abg83395	Human int
65	810	99.8	193	2	Aar99560	Human int
66	810	99.8	193	2	Aaw52172	Interfero
67	810	99.8	193	2	Aaw47429	Interfero
68	810	99.8	193	2	Aaw37740	Interfero
69	810	99.8	193	3	Aay53908	Amino aci
70	810	99.8	193	4	Aab82409	Human int
71	810	99.8	193	8	Adl24278	Human IL-
72	809	99.5	157	6	Abg83403	Human int
73	808	99.5	157	6	Abg83407	Human int
74	808	99.5	157	6	Abg83404	Human int
75	808	99.5	157	6	Abg83402	Human int
76	808	99.5	157	6	Abg83400	Human int
77	808	99.5	157	6	Abg83401	Human int
78	808	99.5	157	6	Abg83394	Human int
79	808	99.5	157	6	Abg83397	Human int
80	808	99.5	193	2	Aaw77082	Interleuk
81	807	99.4	157	6	Abg73367	Human mat
82	807	99.4	157	6	Abg83396	Human int
83	807	99.4	157	6	Abg83398	Human int
84	807	99.4	193	6	Abg73366	Human pre
85	805	99.1	157	6	Abg73364	Human mat
86	805	99.1	157	6	Abg73363	Human int
87	805	99.1	157	6	Abg83408	Human int
88	805	99.1	157	6	Adu49654	Human IL-
89	805	99.1	193	6	Abg73360	Human pre
90	805	99.1	193	6	Abg73361	Human pre
91	805	99.1	325	9	Ady22168	Human IL-
92	805	99.1	361	9	Ady22166	Human IL-
93	803	98.9	157	7	Aae39507	Human mat
94	803	98.9	157	8	Adu49656	Human IL-
95	803	98.9	193	2	Aaw31757	Interfero
96	803	98.9	193	7	Aae39505	Human int
97	801	98.6	157	2	Aaw77083	Human int

98 801 98.6 157 2 AAW48961 Aaw48961 Mutant hu  
99 801 98.6 157 8 ADU06896 Adu06896 Human int  
100 801 98.6 181 3 AAB23797 Aab23797 Human int

## ALIGNMENTS

RESULT 1  
AAW77077  
ID AAW77077 standard; peptide; 157 AA.  
XX  
AC AAW77077;  
XX  
DT 16-NOV-1998 (first entry)  
XX  
DE Human interleukin 18.  
XX  
DE Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.  
XX  
OS Homo sapiens.  
XX  
PN EP861663-A2.  
XX  
PD 02-SEP-1998.  
XX  
PF 24-FEB-1998; 98EP-00301352.  
XX  
PR 25-FEB-1997; 97JP-00055468.  
XX  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
PI Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;  
XX  
DR WPI; 1998-448964/39.  
XX  
DR N-PSDB; AAW48226.  
XX  
PT Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
XX e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism  
XX and osteoporosis.  
XX  
PS Claim 4; Page 18; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for  
XX inhibition of osteoclast formation. IL-18 is used for treating or  
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
CC osteoporosis  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 2; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 2

AAYS7570  
ID AAYS7570 standard; protein; 157 AA.  
XX  
AC AAYS7570;  
XX  
DT 06-MAR-2000 (first entry)  
XX  
DE Human interleukin 18 protein sequence SEQ ID NO:1.  
XX  
KW Human; interleukin 18; IL-18; potentiator; IGF; tumour; cancer;  
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO9959565-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US011160.  
XX  
PR 21-MAY-1998; 98US-0086560P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Johnson RK;  
XX  
DR WPI; 2000-062368/05.  
XX  
PT New polypeptides, useful for preparation of composition for preventing  
XX and/or treating cancer by inhibiting tumor growth.  
XX  
PS Claim 1; Page 49-50; 53pp; English.

XX The present sequence represents human interleukin 18 (IL-18). The present  
CC invention describes a compound comprising human or murine IL-18 in  
CC combination with a chemotherapeutic agent (I). Also described are: (1) a  
CC method of preventing and/or treating cancer in a mammal comprising the  
CC administration of a cancer inhibiting amount of (I) comprising the IL-18  
CC protein and the chemotherapeutic agent and optionally a pharmaceutically  
CC acceptable carrier; and (2) a method of inhibiting the growth of tumour  
CC cells in a mammal sensitive to a composition comprising human IL-18  
CC and/or murine IL-18 and the chemotherapeutic agent (and optionally a  
CC pharmaceutically acceptable carrier), comprising administering to a  
CC mammal afflicted with the tumour cells an effective tumour cell growth  
CC inhibiting amount of (I). The IL-18 protein in conjunction with a  
CC chemotherapeutic agent is useful in a method for preventing and/or  
CC treating cancer in mammals by inhibiting the growth of tumours or  
CC cancerous cells in mammals  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 3; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120  
DB 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 3  
AAG65351  
ID AAG65351 standard; protein; 157 AA.  
XX  
AC AAG65351;

```
XX 30-NOV-2001 (first entry)
DT Human interleukin-18 (IL-18) protein fragment.
XX
XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW neutropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX
XX Homo sapiens.
OS
XX WO200158956-A2.
PN
XX 16-AUG-2001.
PD
XX 09-FEB-2001; 2001WO-US004170.
PF
XX 10-FEB-2000; 2000US-0181608P.
PR
XX (BADI ) BASF AG.
PA
XX Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
PI
XX WPI; 2001-550020/61.
DR
XX Novel antibodies and compounds capable of binding to human interleukin-18
PT useful for treating, e.g., inflammatory disorders, neurological
PT disorders, heart failure, myocardial infarction, and autoimmune diseases.
XX
XX Disclosure; Page 14; 91pp; English.
PS
XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents a human IL-18 protein fragment
XX
XX Sequence 157 AA;
SQ
Query Match 99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 1:5e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVCKEIKSLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Db 61 AVTISVCKEIKSLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
RESULT 4
AAG65294
ID AAG65294 standard; protein; 157 AA.
XX
XX AAG65294;
AC
```

```
XX 30-NOV-2001 (first entry)
DT Human interleukin-18 (IL-18) protein fragment.
XX
XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW neutropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX
XX Homo sapiens.
OS
XX WO200158956-A2.
PN
XX 16-AUG-2001.
PD
XX 09-FEB-2001; 2001WO-US004170.
PF
XX 10-FEB-2000; 2000US-0181608P.
PR
XX (BADI ) BASF AG.
PA
XX Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
PI
XX WPI; 2001-550020/61.
DR
XX Novel antibodies and compounds capable of binding to human interleukin-18
PT useful for treating, e.g., inflammatory disorders, neurological
PT disorders, heart failure, myocardial infarction, and autoimmune diseases.
XX
XX Disclosure; Page 9; 91pp; English.
PS
XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents a human IL-18 protein fragment
XX
XX Sequence 157 AA;
SQ
Query Match 99.9%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 1:5e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVCKEIKSLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Db 61 AVTISVCKEIKSLSCENKIIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDNKMOPESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
RESULT 5
AAE06661
ID AAE06661 standard; protein; 157 AA.
XX
XX AAE06661;
AC
```

XX 16-OCT-2001 (first entry)  
XX Human interleukin-1gamma (IL-1gamma) protein.  
XX Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;  
XX immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.  
XX  
OS Homo sapiens.  
XX WO200157219-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 01-FEB-2001; 2001WO-US003285.  
XX  
XX 02-FEB-2000; 2000US-0179638P.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
XX WPI; 2001-488886/53.  
XX  
XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
XX polypeptide useful for treating conditions exhibiting abnormal expression  
XX of interleukin such as immunological disorders, tumor and allergy.  
XX  
XX Disclosure; Fig 1; 103pp; English.  
XX  
XX The invention relates to recombinant antigenic interleukin-1 like  
XX molecules and their corresponding nucleic acid sequences, designated as  
XX interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL  
XX -1delta and IL-1epsilon are useful for treating conditions exhibiting  
XX abnormal expression of the interleukin such as immunological disorders,  
XX tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,  
XX allergy, autoimmune diseases and infectious diseases (e.g., pulmonary  
XX tuberculosis, leprosy, fulminant hepatitis, and viral infections such as  
XX HIV). The invention also relates to methods of using the composition  
XX containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic  
XX utilities. IL-1delta is used as an immunogen for the production of  
XX antisera or antibodies specific, e.g., capable of distinguishing between  
XX IL-1 family members and an IL-1delta, for the interleukin or its  
XX fragment. The purified interleukin is used as a reagent to detect any  
XX antibodies generated in response to the presence of elevated levels of  
XX expression, or immunological disorders which lead to antibody production  
XX to the endogenous cytokine. The invention also contemplates the use of  
XX competitive drug screening assays. The present sequence is human  
XX interleukin-1gamma (IL-1gamma) protein related to the invention  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKKQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKKQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 6  
ABB04389  
  
Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKKQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKKQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 6  
ABB04389

ID ABB04389 standard; protein; 157 AA.  
XX  
AC ABB04389;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Human IL-18.  
XX  
KW Human; IL-18; interleukin-18; cancer.  
XX  
OS Homo sapiens.  
XX  
PN CN1326992-A.  
XX  
PD 19-DEC-2001.  
XX  
PF 07-JUN-2000; 2000CN-00107993.  
XX  
PR 07-JUN-2000; 2000CN-00107993.  
XX  
PA (SHUA-) SHUANGLU PHARM CO LTD BEIJING.  
XX  
PI Xu M, Wang Y, Huang X;  
XX  
DR WPI; 2002-217571/28.  
DR N-PSDB; ABL41315.  
XX  
XX Gene cloning, product preparation and use of Chinese interleukin-18  
XX subype (53 Arg IL-18), useful for treating of cancer and other disease.  
XX  
PS Claim 1; Page 7 (Disclosure); 8pp; Chinese.  
XX  
CC The invention relates to the preparation of recombinant human interleukin  
XX -18 for treating of cancer and other disease  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKKQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFORSVPGHDNKKQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 7  
AAE17134  
ID AAE17134 standard; protein; 157 AA.  
XX  
AC AAE17134;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human IL-18 protein.  
XX  
KW Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV;  
KW influenza virus; human immunodeficiency virus; HIV; herpes simplex virus;  
KW hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus;  
KW HPV; hepatitis C virus; HCV.  
XX  
OS Homo sapiens.  
XX  
PN WO200193898-A1.  
XX





XX WPI; 2003-298731/29.  
 DR N-PSDB; ABX11788.  
 XX  
 XX Novel interleukin-18 mutant polypeptide useful in the treatment of cancer  
 PT and viral disease, has mutations in amino acid residues which are  
 PT involved in its interaction with IL-18 binding protein.  
 XX  
 PS Example 1; Fig 1B; 23pp; English.  
 XX  
 CC The present invention relates to mutants of human interleukin-18 (IL-18)  
 CC protein that have a lower affinity for IL-18 binding protein (IL-18BP)  
 CC than the wild-type IL-18 protein. The IL-18 mutants of the invention  
 CC comprise mutations in one or more amino acid residues which are involved  
 CC in its interaction with IL-18BP. The mutations comprise substitutions,  
 CC preferably non-conservative, additions or deletions. A pharmaceutical  
 CC composition comprising an IL-18 mutant is useful for treating a disease  
 CC which is prevented or alleviated by a T helper type 1 (Th1) response,  
 CC including cancer and viral disease. The IL-18 mutants are useful in the  
 CC treatment of the above diseases, microbial infections, in tumour  
 CC immunotherapy, and as an adjuvant in DNA vaccination and in graft versus  
 CC tumour therapy. The IL-18 mutants are resistant to, or less susceptible  
 CC to, neutralisation than the wild-type protein. The present sequence  
 CC represents human wild-type mature IL-18 protein  
 XX  
 SQ Sequence 157 AA;  
 Query Match 99.9%; Score 811; DB 6; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNPRTTIFIIISMVKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNPRTTIFIIISMVKDSQPRGM 60  
 QY 61 AVTISVKCKISLSCENKIISFKENPPDNINIKDTKSDIIFORSVPGHDNKKMOFESSY 120  
 DB 61 AVTISVKCKISLSCENKIISFKENPPDNINIKDTKSDIIFORSVPGHDNKKMOFESSY 120  
 QY 121 EGYFLACERDLFKLILKKEDELGRSINFVTQVED 157  
 DB 121 EGYFLACERDLFKLILKKEDELGRSINFVTQVED 157  
 RESULT 10  
 ADA50616  
 ID ADA50616 standard; protein; 157 AA.  
 XX  
 AC ADA50616;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 XX Human mature consensus interleukin-18 (IL-18), SEQ ID NO:71.  
 DE  
 DE Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
 KW humoral response; cellular response; immune response; immunotherapy;  
 KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 4  
 FT /note= "Glu may replace wild-type Lys in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 5  
 FT /note= "Val may replace wild-type Leu in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 6  
 FT /note= "Ile may replace wild-type Glu in a variant  
 FT protein. A variant protein with this substitution would

FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 8  
 FT /note= "Asp may replace wild-type Lys in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 10  
 FT /note= "Thr may replace wild-type Ser in a variant  
 FT protein. A variant protein with this substitution would  
 FT not have changed immunogenicity compared to the wild-type  
 FT protein"  
 FT  
 FT Misc-difference 12  
 FT /note= "Val may replace wild-type Ile in a variant  
 FT protein. A variant protein with this substitution would  
 FT not have changed immunogenicity compared to the wild-type  
 FT protein"  
 FT  
 FT Misc-difference 13  
 FT /note= "Ile may replace wild-type Arg in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 15  
 FT /note= "Arg may replace wild-type Leu in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 17  
 FT /note= "Lys may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 20  
 FT /note= "Val or Ile may replace wild-type Leu in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 21  
 FT /note= "Tyr may replace wild-type Phe in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 22  
 FT /note= "Val may replace wild-type Ile in a variant  
 FT protein. A variant protein with this substitution is  
 FT unlikely to have changed immunogenicity compared to the  
 FT wild-type protein"  
 FT  
 FT Misc-difference 27  
 FT /note= "Lys may replace wild-type Arg in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 30  
 FT /note= "Ala may replace wild-type Phe in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 35  
 FT /note= "Lys may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 37  
 FT /note= "Phe may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 38  
 FT /note= "Glu may replace wild-type Cys in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 39  
 FT /note= "Ala may replace wild-type Arg in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 40  
 FT /note= "Trp may replace wild-type Asp in a variant  
 FT protein. A variant protein with this substitution would  
 FT have changed activity compared to the wild-type protein"  
 FT  
 FT Misc-difference 45  
 FT /note= "Ser may replace wild-type Thr in a variant  
 FT protein. A variant protein with this substitution would

FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 47  
FT /note= "Tyr may replace wild-type Phe in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 51  
FT /note= "Glu may replace wild-type Met in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 52  
FT /note= "Phe may replace wild-type Tyr in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 53  
FT /note= "Gly may replace wild-type Lys in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 56  
FT /note= "Ile may replace wild-type Glp in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 58  
FT /note= "Ala may replace wild-type Arg in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 62  
FT /note= "Lys may replace wild-type Val in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 64  
FT /note= "Val may replace wild-type Ile in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 94  
FT /note= "Lys may replace wild-type Asp in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 95  
FT /note= "Phe may replace wild-type Thr in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 101  
FT /note= "Tyr may replace wild-type Phe in a variant  
FT protein. A variant protein with this substitution would  
FT not have changed immunogenicity compared to the wild-type  
FT protein"  
FT Misc-difference 104  
FT /note= "Leu may replace wild-type Arg in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 108  
FT /note= "Ile may replace wild-type Gly in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 111  
FT /note= "Lys may replace wild-type Asn in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 129  
FT /note= "Phe may replace wild-type Lys in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 131  
FT /note= "Asp may replace wild-type Arg in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 132  
FT /note= "Leu may replace wild-type Asp in a variant  
FT protein. A variant protein with this substitution would

FT Misc-difference 133  
FT /note= "Glu may replace wild-type Leu in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
FT Misc-difference 134  
FT /note= "Ala may replace wild-type Phe in a variant  
FT protein. A variant protein with this substitution would  
FT have changed activity compared to the wild-type protein"  
PN WO2003031569-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 18-SEP-2002; 2002WO-US029640.  
XX  
PR 10-OCT-2001; 2001US-0328371P.  
XX (CENZ ) CENTOCOR INC.  
XX Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;  
PI Branigan PJ;  
XX WPI; 2003-393437/37.  
DR N-PSDB; ADA50613.  
XX  
FT New nucleic acid vaccine, useful for eliciting an immune response to a  
Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60  
Qy 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQKSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQKSVPGHDKMQFESSY 120  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFVTQNE 157  
RESULT 11  
ADA50610  
ID ADA50610 standard; protein; 157 AA.  
XX  
AC ADA50610;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human mature consensus interleukin-18 (IL-18), SEQ ID NO:65.  
XX  
KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
KW humoral response; cellular response; immune response; immunotherapy;  
KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003031569-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 18-SEP-2002; 2002WO-US029640.  
XX  
PR 10-OCT-2001; 2001US-0328371P.  
XX (CENZ ) CENTOCOR INC.  
XX Snyder L, Scallon B, Knight DM, Mccarthy SG, Goletz TJ;  
PI Branigan PJ;

XX WPI; 2003-393437/37.  
DR N-PSDB; ADA50608.  
XX  
XX New nucleic acid vaccine, useful for eliciting an immune response to a  
PT cancer associated tumor protein in a mammal.  
PT  
XX Claim 1b; Page 51-52; 92pp; English.  
PS  
XX The invention relates to a nucleic acid vaccine comprising one or more  
CC tumor antigen-encoding nucleic acids and one or more cytokine adjuvant-  
CC encoding nucleic acids. The tumor antigen encoded by the vaccine is  
CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,  
CC also known as KUK3), and the cytokine adjuvant encoded can be interleukin  
CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),  
CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid  
CC is preferably under the control of a promoter such as the cytomegalovirus  
CC immediate early promoter, the dihydrofolate reductase promoter or the  
CC early or late SV40 promoters. The invention also encompasses the method  
CC of eliciting an immune response to a tumour antigen in a mammal using the  
CC vaccine of the invention. Coexpression of the antigen and adjuvant  
CC induces a humoral or cellular response to the tumour antigen, generating  
CC an immune response useful for treatment or prophylaxis of cancers. The  
CC present sequence represents an interleukin-18 (IL-18) polypeptide which  
CC is specifically claimed for use in the vaccine of the invention.  
XX  
SQ Sequence 157 AA;  
Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60  
QY 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
RESULT 13  
ABR83372  
ID ABR83372 standard; protein; 157 AA.  
XX ABR83372;  
AC ABR83372;  
XX 07-OCT-2003 (first entry)  
DT Human interleukin 18 amino acid sequence.  
DE  
XX Human; interleukin 1; IL-1; interleukin 18; IL-18; mutant; mutein;  
KW mutant interleukin 18; MUT-IL-18; antiinflammatory; gene therapy;  
KW inflammatory disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO2003057821-A2.  
FN  
XX 17-JUL-2003.  
PD  
XX 25-OCT-2002; 2002WO-US034235.  
PF  
XX 26-OCT-2001; 2001US-0335880P.  
PR (CENZ ) CENTOCOR INC.  
XX Heavner GA, Snyder LA, McCarthy SG;  
PA  
XX  
PI  
XX

DR WPI; 2003-577517/54.  
XX  
XX New MUT-IL-18 nucleic acid, useful for preparing a composition for  
PT diagnosing or treating a MUT-IL-18 related condition, e.g., inflammatory  
PT disorder.  
XX  
PS Example 3; Page 74; 97pp; English.  
XX  
XX The present invention describes a mutant interleukin 18 (MUT-IL-18)  
CC nucleic acid comprising or complementary to at least one polynucleotide  
CC encoding an IL-18 amino acid sequence comprising at least one mutation  
CC corresponding to at least one substitution selected from the group  
CC consisting of Thr10 for Ser10, Val12 for Ile12, Ser45 for Thr45, Tyr47  
CC for Phe47, Phe52 for Tyr52, Val64 for Ile64, Tyr101 for Phe101, Val15 for  
CC Leu5, Val20 for Leu20, Ile20 for Leu20, Tyr21 for Phe21, Val22 for Ile22,  
CC Ile66 for Val66, Thr72 for Ser72, or Phe148 for Ser148. Also described:  
CC (1) a MUT-IL-18 polypeptide; (2) a MUT-IL-18 antibody; (3) a MUT-IL-18  
CC vector comprising the MUT-IL-18 nucleic acid; (4) a MUT-IL-18 host cell  
CC comprising the MUT-IL-18 nucleic acid; (5) a composition comprising a MUT  
CC -IL-18 nucleic acid, polypeptide or antibody; (6) diagnosing or treating  
CC a MUT-IL-18 related condition in a cell, tissue, organ or animal; (7) a  
CC device comprising MUT-IL-18 nucleic acid, polypeptide or antibody and  
CC that is suitable for contacting or administering the MUT-IL-18 nucleic  
CC acid, polypeptide or antibody; (8) an article of manufacture for human  
CC pharmaceutical or diagnostic use; and (9) producing the MUT-IL-18 nucleic  
CC acid, polypeptide or antibody. MUT-IL-18 has antiinflammatory activity  
CC and can be used in gene therapy. The MUT-IL-18 nucleic acid can be used  
CC for preparing a composition for diagnosing or treating a MUT-IL-18  
CC related condition, e.g. inflammatory disorder. The present sequence  
CC represents a human IL-18 amino acid sequence given in an example from the  
CC present invention  
XX  
SQ Sequence 157 AA;  
Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60  
QY 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKDTKSDIIFORSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
RESULT 13  
ADE06775  
ID ADE06775 standard; protein; 157 AA.  
XX ADE06775;  
AC ADE06775;  
XX 29-JAN-2004 (first entry)  
DT Human anti-diabetes Ig derived protein SEQ ID NO:3.  
DE  
XX human; Ig; diabetes; complementarity-determining region; CDR;  
KW antidiabetic; ophthalmological; neuroprotective; gene therapy;  
KW diabetes mellitus; insulin resistance; hyperglycaemia; hypoglycaemia;  
KW pancreatitis; Cushing's syndrome; acanthosis nigricans; retinopathy;  
KW nephropathy; polyneuropathy; ulcer; infection.  
XX  
XX Homo sapiens.  
OS  
XX WO2003083071-A2.  
FN  
XX 09-OCT-2003.  
PD  
XX

PF 26-MAR-2003; 2003WO-US009459.  
XX  
PR 26-MAR-2002; 2002US-0367902P.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Griswold DE, Li J, Li L;  
XX  
XX WPI; 2003-804047/75.  
DR  
XX  
XX New isolated anti-diabetes immunoglobulin (Ig)-derived protein,  
PT comprising at least one complementarity determining region (CDR) useful  
PT for treating a diabetes-related condition, e.g. type I or II diabetes  
PT mellitus, retinopathy.  
XX  
XX Claim 1; SEQ ID NO 3; 84pp; English.  
XX  
XX The invention relates to a novel isolated anti-diabetes immunoglobulin  
CC (Ig)-derived protein, comprising at least one complementarity-determining  
CC region (CDR). A protein of the invention has antidiabetic,  
CC ophthalmological, and neuroprotective activity, and may have a use in  
CC gene therapy. The protein, nucleic acid, composition and methods of the  
CC invention are useful for treating a diabetes-related condition, e.g. type  
CC I or II diabetes mellitus, insulin resistance, hyperglycaemia,  
CC hypoglycaemia, pancreatitis, Cushing's syndrome, acanthosis nigricans,  
CC retinopathy, nephropathy, polyneuropathy, ulcers, or infections. The  
CC present sequence represents an anti-diabetes Ig derived protein of the  
CC invention.  
XX  
XX Sequence 157 AA;  
SQ

Query Match 99.9%; Score 811; DB 7; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCEKNKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 14  
ADH54826  
ID ADH54826 standard; protein; 157 AA.  
XX  
XX ADH54826;  
AC  
XX  
XX 25-MAR-2004 (first entry)  
DT  
XX  
XX Human interleukin-18 (IL-18).  
DE  
XX  
XX Human; interleukin-18; IL-18; interferon-gamma-inducing factor; IGIF;  
KW Thi-inducer; cytokine; cell-mediated immunity; prevention;  
KW inflammatory bowel disease; IBD; Crohn's disease; ulcerative colitis;  
KW inflammatory colitis; antiinflammatory; gastrointestinal.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004002519-A1.  
PN  
XX  
XX 08-JAN-2004.  
PD  
XX  
XX 05-JUN-2003; 2003WO-US017744.  
PF  
XX  
XX 27-JUN-2002; 2002US-0392176P.  
PR  
XX

PA (SMIX ) SMITHKLINE BEECHAM CORP.  
XX  
XX Goto Y, Kikkawa H, Kinoshita M;  
XX  
XX WPI; 2004-099186/10.  
DR  
XX  
XX Preventing and/or treating inflammatory bowel diseases caused by  
PT bacteria, ischemia, radiation, drugs or chemical substances comprises  
PT administering an interferon-gamma-inducing factor (IGIF), interleukin-18.  
XX  
XX Claim 1; SEQ ID NO 1; 20pp; English.  
PS  
XX  
XX The invention relates to a method of treating or preventing inflammatory  
CC bowel disease (IBD) by administering human or murine interleukin-18 (IL-  
CC 18; ADH54826-ADH54827). The invention also relates to a pharmaceutical  
CC composition comprising human or murine IL-18 for treating or preventing  
CC IBD. IL-18 (also known as interferon-gamma-inducing factor (IGIF)) is a  
CC potent Thi-inducing cytokine and thus plays a key role in cell-mediated  
CC immunity. The methods and compositions of the invention are useful for  
CC the prevention and/or treatment of IBD, including Crohn's disease,  
CC ulcerative colitis and inflammatory colitis caused by bacteria, ischemia,  
CC radiation, drugs or chemical substances. The present sequence represents  
CC human IL-18 which is specifically claimed for use in the methods and  
CC compositions of the invention.  
XX  
XX Sequence 157 AA;  
SQ

Query Match 99.9%; Score 811; DB 8; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQFESSY 120  
Db 61 AVTISVKCEKISTLSCEKNKIIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 15  
ADL24279  
ID ADL24279 standard; protein; 157 AA.  
XX  
XX ADL24279;  
AC  
XX  
XX 03-JUN-2004 (first entry)  
DT  
XX  
XX Human IL-18 ICE-processed.  
DE  
XX  
XX cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;  
KW antagonist.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004019866-A2.  
PN  
XX  
XX 11-MAR-2004.  
PD  
XX  
XX 21-AUG-2003; 2003WO-US026354.  
PF  
XX  
XX 28-AUG-2002; 2002US-0406418P.  
PR  
XX  
XX 12-AUG-2003; 2003US-0494457P.  
XX  
XX (IMMV ) IMMUNEX CORP.  
PA  
XX  
XX Burton PB, Deisher TA;  
PI  
XX  
XX WPI; 2004-239107/22.  
DR

XX Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a  
PT cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
PT failure, aneurysm, angina, embolism, restenosis, ischemia or  
XX thrombocytopenic purpura.  
PS Disclosure; Page 112; 135pp; English.  
XX  
CC The present invention relates to a method of treating cardiovascular  
CC disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
CC CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
CC antagonists are useful for treating cardiovascular disorders, e.g.  
CC (chronic immune) myocarditis, congestive heart failure, aneurysms,  
CC angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
CC present sequence is a polypeptide used in the exemplification of the  
XX invention.  
XX Sequence 157 AA;  
Query Match 99.9%; Score 811; DB 8; Length 157;  
Best Local Similarity 99.4%; Pred. No. 1.5e-82;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60  
QY -61 AVTISVKCEKISXLSCKENKIIISPKENPPDNIKDTKSDIIFORSVPGHDKMKQFESSY 120  
DB 61 AVTISVKCEKISXLSCKENKIIISPKENPPDNIKDTKSDIIFORSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157  
Search completed: January 30, 2006, 08:37:18  
Job time : 137 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:48:54 ; Search time 167 Seconds  
(without alignments)  
663.281 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 157

Sequence: 1 YFGKLESLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNEED 157

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	53.5	189	2	Q6WJ17_HUMAN
2	84	53.5	193	1	IL18_HUMAN
3	84	53.5	193	2	Q6FGF3_HUMAN
4	55	35.0	193	2	Q96KJ8_HUMAN
5	54	34.4	193	2	Q9BG15_MACMU
6	39	24.8	45	2	Q9NQ49_HUMAN
7	19	12.1	159	2	Q6QVC4_CAPHI
8	19	12.1	193	2	Q9GL09_SHEEP
9	14	8.9	178	2	Q9MZL8_BOVIN
10	14	8.9	193	1	IL18_BOVIN
11	14	8.9	193	2	Q5I931_BOSTR
12	14	8.9	193	2	Q6TLW4_BUBBU
13	14	8.9	193	2	Q6T573_BUBBU
14	13	8.3	177	2	Q6STL7_PIG
15	13	8.3	192	1	IL18_PIG
16	13	8.3	192	2	Q865B8_FELCA
17	13	8.3	192	2	Q9N1P7_PIG
18	13	8.3	192	2	Q95M33_FELCA
19	13	8.3	193	1	IL18_CANFA
20	13	8.3	193	1	IL18_HORSE
21	10	6.4	84	2	Q95LE7_CANFA
22	8	5.1	195	2	Q80X07_MERUN
23	8	5.1	660	2	Q5T9T7_HUMAN
24	8	5.1	893	2	Q68D55_HUMAN
25	8	5.1	1139	1	ARHGA_HUMAN
26	8	5.1	2175	2	Q5S003_MOUSE
27	8	5.1	2223	2	Q6Q759_HUMAN
28	8	5.1	5890	2	Q8IK84_PLAF7
29	7	4.5	61	2	Q6IGT1_DROME
30	7	4.5	128	2	Q4JAC8_SULAC
31	7	4.5	144	2	Q77LV3_GNUCL

32	7	4.5	144	2	Q9E215_GNUCL
33	7	4.5	144	2	Q91F19_GNUCL
34	7	4.5	145	2	Q9HL54_TREAC
35	7	4.5	151	2	Q8CZ29_STRRG
36	7	4.5	151	2	Q97S21_STRPN
37	7	4.5	158	2	Q98RY8_GUITH
38	7	4.5	164	2	Q4FT23_9THEM
39	7	4.5	170	2	Q5AR78_EMENI
40	7	4.5	181	2	Q620C0_CAEBR
41	7	4.5	188	2	Q34259_9HEMI
42	7	4.5	189	2	Q35368_9HEMI
43	7	4.5	189	2	Q80S88_MOUSE
44	7	4.5	190	2	Q8WBS8_9HEMI
45	7	4.5	192	1	IL18_MOUSE
46	7	4.5	192	2	Q6USQ6_MOUSE
47	7	4.5	196	2	Q91266_SIGHI
48	7	4.5	206	2	Q81UB6_BACAN
49	7	4.5	212	2	Q612K1_BACAN
50	7	4.5	221	2	Q4XGS4_PLACH
51	7	4.5	231	2	Q6YIH6_MYRFP
52	7	4.5	242	2	Q73LC6_TREDE
53	7	4.5	246	2	Q82652_ARATH
54	7	4.5	254	2	Q91FD9_IRV6
55	7	4.5	259	2	Q4Z9D4_9CAUD
56	7	4.5	264	2	Q4ZXZ7_PSESY
57	7	4.5	268	2	Q7V2J4_PROMP
58	7	4.5	275	2	Q4IRQ9_GIBZE
59	7	4.5	285	2	Q7UE74_RHOBA
60	7	4.5	292	2	Q9KEQ4_CABEL
61	7	4.5	325	2	Q9KEQ4_BACHD
62	7	4.5	334	2	Q74M41_NANEO
63	7	4.5	326	2	Q97UH2_SULSO
64	7	4.5	329	2	Q9GQ96_PLAFA
65	7	4.5	329	2	Q9CJT5_PASMU
66	7	4.5	333	2	Q9GQ94_PLAFA
67	7	4.5	334	2	Q92XB4_RHIME
68	7	4.5	334	2	Q835H8_ENTFA
69	7	4.5	366	2	Q8RA01_THETN
70	7	4.5	390	2	Q8FUG3_ECOL6
71	7	4.5	393	2	Q6AAL3_PROAC
72	7	4.5	417	2	Q5FL86_LACAC
73	7	4.5	429	1	ENO_ANAP
74	7	4.5	431	2	Q5NLS8_ORYSA
75	7	4.5	432	1	ENO_SYNY3
76	7	4.5	435	2	Q6FIR7_MESFL
77	7	4.5	449	2	Q7TTV6_SYNPX
78	7	4.5	458	2	Q22803_ARATH
79	7	4.5	465	2	Q8VY01_ARATH
80	7	4.5	484	2	Q7PXA5_ANOGA
81	7	4.5	496	2	Q5JMA8_ORYSA
82	7	4.5	510	2	Q73Y86_MYCPA
83	7	4.5	525	2	Q8IIC0_PLAF7
84	7	4.5	525	2	Q8IIC0_PLAF7
85	7	4.5	547	2	Q4SPA4_TETNG
86	7	4.5	548	2	Q9RA74_STRDY
87	7	4.5	552	1	NCAP_FPMV
88	7	4.5	557	2	Q7XVA4_ORYSA
89	7	4.5	589	2	Q8MM81_CABEL
90	7	4.5	612	2	Q5HBG0_EHRW
91	7	4.5	614	2	Q73RP0_TREDE
92	7	4.5	618	2	Q5ATS8_EMENI
93	7	4.5	623	2	Q6LK80_PHOPR
94	7	4.5	624	2	Q9UJN7_CABEL
95	7	4.5	633	2	Q5FHN3_EHRWG
96	7	4.5	633	2	Q5FDV4_EHRW
97	7	4.5	641	1	LICR_BACSU
98	7	4.5	645	2	Q6CV48_KLULA
99	7	4.5	653	2	Q4FV41_9GAMM
100	7	4.5	653	2	Q6F741_AC1AD

ALIGNMENTS

Q77LV3 helicoverpa

Q9E215 helicoverpa  
Q91F19 helicoverpa  
Q9HL54 thermoplasm  
Q8CZ29 streptococc  
Q97S21 streptococc  
Q98RY8 quillardia  
Q4FT23 thermotoga  
Q5AR78 aspergillus  
Q620C0 caenorhabdi  
Q34259 chaitoregma  
Q35368 pseudoregma  
Q80S88 mus musculu  
Q8WBS8 chaitophoru  
P70380 mus musculu  
Q6USQ6 mus musculu  
Q91266 sigmodon hi  
Q81UB6 bacillus an  
Q612K1 bacillus an  
Q4XGS4 plasmodium  
Q5YIH6 myrmecia py  
Q73LC6 treponema d  
Q82652 arabidopsis  
Q91FD9 chilo iride  
Q4Z9D4 staphylococ  
Q4ZXZ7 pseudomonas  
Q7V2J4 prochloroco  
Q4IRQ9 gibberella  
Q7UE74 rhodopirell  
Q9KEQ4 caenorhabdi  
Q74M41 nanoarchaeu  
Q97UH2 sulfolobus  
Q9GQ96 plasmodium  
Q9CJT5 pasteurrella  
Q9GQ94 plasmodium  
Q92XB4 rhizobium m  
Q835H8 enterococcu  
Q8RA01 thermoanaer  
Q8FUG3 escherichia  
Q6AAL3 propionibac  
Q5FL86 lactobacill  
Q8YR80 anabaena sp  
Q5NLS8 oryza sativ  
Q77972 synechocyst  
Q6FIR7 mesoplasma  
Q7TTV6 synechococc  
Q22803 arabidopsis  
Q8VY01 arabidopsis  
Q7PXA5 anopheles g  
Q5JMA8 oryza sativ  
Q73Y86 mycobacteri  
Q8IIC0 plasmodium  
Q7WT34 streptomyc  
Q4SPA4 tetraodon n  
Q9RA74 streptococc  
Q9W840 tupia para  
Q7XVA4 oryza sativ  
Q8MM81 caenorhabdi  
Q5HBG0 ehrlichia r  
Q73RP0 treponema d  
Q5ATS8 aspergillus  
Q6LK80 photobacter  
Q9UJN7 caenorhabdi  
Q5FHN3 ehrlichia r  
Q5FDV4 ehrlichia r  
P46321 b probable  
Q6CV48 kluyveromyc  
Q4FV41 psychrobact  
Q6F741 acinetobact

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RESULT 1
ID Q6WJ7_HUMAN PRELIMINARY; PRT; 189 AA.
AC Q6WJ7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE DELTA3PRO-IL-18.
GN Name=IL18;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaggero A., De Ambrosis A., Mezzanzanica D., Piazza T., Rubartelli A.,
RA Figini M., Canevari S., Ferrini S.;
RT "A novel isoform of pro-interleukin-18 expressed in ovarian tumors is
RT resistant to caspase-1 and -4 processing.";
RL Oncogene 0:0(2004).
DR EMBL; AY266351; AAP92112.1; -; mRNA.
DR SMR; Q6WJ7; 33-189.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Sequence 189 AA; 21896 MW; A8BA275CF713A4B6 CRC64;
SQ
Query Match 53.5%; Score 84; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 LSCENKIISFKENMPDNIDKTSIDIFQRSVPGHNDKMQPSSSYEGYFLACEKERDL 133
Db 106 LSCENKIISFKENMPDNIDKTSIDIFQRSVPGHNDKMQPSSSYEGYFLACEKERDL 165
QY 134 FKILKKEDELGRSMFTVQNEED 157
Db 166 FKILKKEDELGRSMFTVQNEED 189

RESULT 2
IL18_HUMAN STANDARD; PRT; 193 AA.
AC Q14116; O75599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF, IL1F4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Liver;
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein.";
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP NUCLEOTIDE SEQUENCE [MRNA].
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human interleukin 18 cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Urinary bladder;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 2-193.
RC TISSUE=Peripheral blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; D49950; BAA08706.1; -; mRNA.
CC EMBL; AF077611; AAC27787.1; -; mRNA.
CC EMBL; AY044641; AAK95950.1; -; mRNA.
CC EMBL; BC007007; AAH07007.1; -; mRNA.
CC EMBL; BC007461; AAH07461.1; -; mRNA.
CC EMBL; U90434; AAB50010.1; -; mRNA.
CC FDB; J305; NMR; A=37-193.
CC OGP; Q14116; -.
CC Ensembl; ENSG00000150782; Homo sapiens.
CC HGNC; HGNC:5986; IL18.
CC H-InvDB; HIX0010123; -.
CC MIM; 600953; -.
CC GO; GO:0005576; C:extracellular region; TAS.
CC GO; GO:0005125; F:cytokine activity; TAS.
CC GO; GO:0004871; F:signal transducer activity; TAS.
CC GO; GO:0001525; P:angiogenesis; IDA.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0042033; P:chemokine biosynthesis; TAS.
CC GO; GO:0042233; P:granulocyte macrophage colony-stimulating f. .; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISS.
CC GO; GO:0042095; P:interferon-gamma biosynthesis; TAS.
CC GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
CC GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.
CC GO; GO:0042104; P:positive regulation of activated T cell pro. .; IDA.
CC GO; GO:0030155; P:regulation of cell adhesion; IDA.
CC GO; GO:0030431; P:sleep; ISS.
CC GO; GO:0042092; P:T-helper 2 type immune response; TAS.

```



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DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR SMART: SM00125; IL1; 1.
KW 3D-structure; Cytokine.
FT PROPEP 1 36
FT CHAIN 37 193
FT CHAIN 37 193
FT CONFLICT 66 66
FT CONFLICT 86 86
FT CONFLICT 191 191
FT CONFLICT 191 191
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;
Query Match 53.5%; Score 84; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.2e-83;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 LSCENKIISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 133
DB 110 LSCENKIISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 169
QY 134 FKLLKKEDELGDRSIMFTVQNE 157
DB 170 FKLLKKEDELGDRSIMFTVQNE 193
RESULT 3
Q6FGY3 HUMAN
ID Q6FGY3 HUMAN PRELIMINARY; PRT; 193 AA.
AC Q6FGY3;
DT 10-MAY-2005 (TremBLrel. 30, Created)
DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
DE IL18 protein.
GN Name=IL18;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541973; CAG46771.1; -; mRNA.
DR EMBL; CR542001; CAG46798.1; -; mRNA.
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;
Query Match 53.5%; Score 84; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.2e-83;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 LSCENKIISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 133
DB 110 LSCENKIISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 169
QY 134 FKLLKKEDELGDRSIMFTVQNE 157
DB 170 FKLLKKEDELGDRSIMFTVQNE 193
RESULT 4
Q96KJ8 HUMAN
ID Q96KJ8 HUMAN PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ying P., Jianxin L.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -; mRNA.
DR HSP; Q14116; IJOS.
DR SMR; Q96KJ8; 37-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006985; P:immune response; IEA.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;
Query Match 35.0%; Score 55; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2e-51;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 QVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGMATISVKCEKIS 72
DB 54 QVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGMATISVKCEKIS 108
RESULT 5
Q9BG15 MACMU
ID Q9BG15 MACMU PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Interleukin-18.
GN Name=IL18;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21229850; PubMed=11311040; DOI=10.1089/107999001750133212;
RA Giavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the interleukin-18 gene from rhesus macaque by the
RT simian immunodeficiency virus does not result in increased viral
RT replication."
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -; mRNA.
DR HSP; Q14116; IJOS.
DR SMR; Q9BG15; 37-193.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;
Query Match 34.4%; Score 54; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-50;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 80 IISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 133
DB 116 IISFKEMNPPDNKOTKSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 169
RESULT 6
Q9NQ49 HUMAN
ID Q9NQ49 HUMAN PRELIMINARY; PRT; 45 AA.
AC Q9NQ49;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
GN Name=IL-18;
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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -; Genomic_DNA.
DR HSSP; Q14116; 1J0S.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
FT NON_TER 1 45
FT NON_TER 45 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 24.8%; Score 39; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLEFDMTSDCR 39
|
Db 7 YFGKLESKLVIRNLNDQVLFIDQGNRPLEFDMTSDCR 45
|

RESULT 7
Q6QVC4 CAPHI
ID Q6QVC4 CAPHI PRELIMINARY; PRT; 159 AA.
AC Q6QVC4;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Interleukin-18 (Fragment)
GN Name=il-18;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Liu W., Sui Z., Zhao H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY524275; AAS13327.1; -; mRNA.
DR SMR; Q6QVC4; 3-159.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 159 AA; 18331 MW; FDCDEAAF15278FFC CRC64;

Query Match 12.1%; Score 19; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNI 92
|
Db 76 LSCENKIISFKEMNPPDNI 94
|

RESULT 8
Q9GL09 SHEEP
ID Q9GL09 SHEEP PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Interleukin-18 (IGIF)
GN Name=il-18;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
```

```
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401033; CAC09326.2; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR SMR; Q9GL09; 37-193.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 12.1%; Score 19; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNI 92
|
Db 110 LSCENKIISFKEMNPPDNI 128
|

RESULT 9
Q9MZL8 BOVIN
ID Q9MZL8 BOVIN PRELIMINARY; PRT; 178 AA.
AC Q9MZL8;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment)
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrl M., Bolin C.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR SMR; Q9MZL8; 22-178.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1 1
FT NON_TER 1 1
FT NON_TER 178 178
SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 8.9%; Score 14; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFQRSVPGHD 110
|
Db 118 SDIIFQRSVPGHD 131
|

RESULT 10
IL18 BOVIN
ID IL18 BOVIN STANDARD; PRT; 193 AA.
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
```

DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)  
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
 GN Name=IL18;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20012648; PubMed=10547157; DOI=10.1089/107999099313118;  
 RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;  
 RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-  
 RT 18 expression in macrophages and its IFN-gamma-inducing activity.";  
 RL J. Interferon Cytokine Res. 19:1169-1177(1999).  
 CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
 CC and stimulates interferon gamma production in T helper type I  
 CC cells (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 CC  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; AF124789; AAF08686.1; -; mRNA.  
 DR SMR; Q9TU73; 37-193.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR SMART; SM00125; IL1; 1.  
 KW Cytokine.  
 FT PROPEP  
 FT CHAIN 1 36 By similarity.  
 FT CHAIN 37 193 Interleukin-18.  
 SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA9C4 CRC64;  
 Query Match 8.9%; Score 14; DB 1; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFFQSVPGHD 110  
 |||||  
 Db 133 SDIIFFQSVPGHD 146

RESULT 11  
 Q51931\_BOSTR PRELIMINARY; PRT; 193 AA.  
 ID Q51931; BOSTR PRELIMINARY; PRT; 193 AA.  
 AC Q51931;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Interleukin-18.  
 OS Boselaphus tragocamelus (Nilgai).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Boselaphus.  
 OX NCBI\_TaxID=9917;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Saini M., Swarup D., Yadav M.P., Singh G.R., Arora B.M., Chandra P.,  
 RA Das D.K., Gupta P.K.;  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY842499; AAW34191.1; -; mRNA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 193 AA; 22130 MW; 75B6671696EEA8D CRC64;  
 Query Match 8.9%; Score 14; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFFQSVPGHD 110  
 |||||  
 Db 133 SDIIFFQSVPGHD 146

RESULT 12  
 Q6TLW4\_BUBBU PRELIMINARY; PRT; 193 AA.  
 ID Q6TLW4; BUBBU PRELIMINARY; PRT; 193 AA.  
 AC Q6TLW4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Interleukin 18.  
 GN Name=IL18;  
 OS Bubalus bubalis (Domestic water buffalo).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bubalus.  
 OX NCBI\_TaxID=89462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chaudhury P., Bera B.C.;  
 RT "Cloning and sequencing of Indian water buffalo interleukin-18 cDNA.";  
 RL Eur. J. Immunogenet. 32:75-78(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chaudhuri P., Bera B.C.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY394479; NAO94552.1; -; mRNA.  
 DR SMR; Q6TLW4; 37-193.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 193 AA; 22176 MW; 66116F198DE94BC4 CRC64;  
 Query Match 8.9%; Score 14; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SDIIFFQSVPGHD 110  
 |||||  
 Db 133 SDIIFFQSVPGHD 146

RESULT 13  
 Q6T573\_BUBBU PRELIMINARY; PRT; 193 AA.  
 ID Q6T573; BUBBU PRELIMINARY; PRT; 193 AA.  
 AC Q6T573;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Interleukin-18.  
 OS Bubalus bubalis (Domestic water buffalo).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bubalus.  
 OX NCBI\_TaxID=89462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Premraj A., Sreskumar E., Rasool T.J.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY436506; AAR29081.1; -; mRNA.  
 DR SMR; Q6T573; 37-193.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 SQ SEQUENCE 193 AA; 22190 MW; 93103E5C62B745DE CRC64;  
 Query Match 8.9%; Score 14; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 97 SDIFFORSVPGHD 110
Db 133 SDIFFORSVPGHD 146

RESULT 14
Q6STL7_PIG PRELIMINARY; PRT; 177 AA.
AC Q6STL7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Interleukin 18.
GN Names-IL-18;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lu X., Hui L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY450287; AR27432.1; -; mRNA.
DR SNR; Q6STL7.36-177.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
SQ SEQUENCE 177 AA; 20300 MW; 426F30330EB1F815 CRC64;

Query Match 8.3%; Score 13; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 SDIFFORSVPGHD 110
Db 133 SDIFFORSVPGHD 145

RESULT 15
IL18_PIG STANDARD; PRT; 192 AA.
AC Q19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name-IL18; Synonyms=IGIF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20260994; PubMed=10803849; DOI=10.1007/s002510050630;
RA Fournout S., Dozois C.M., Yerle M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18."

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RL Immunogenetics 51:358-365(2000).
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type 1
CC cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U68701; AAC18415.1; -; mRNA.
DR EMBL; Y11132; CAA72014.1; -; mRNA.
DR EMBL; AB010003; BAA24135.1; -; mRNA.
DR EMBL; AF191088; AAF71200.1; -; mRNA.
DR SMR; O19073; 36-192.
DR GO; GO:0005576; C:extracellular region; ISS.
DR GO; GO:0005125; P:cytokine activity; IMP.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T cell pro. .; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35 BY similarity.
FT CHAIN 36 192 Interleukin-18.
SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 8.3%; Score 13; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 SDIFFORSVPGHD 110
Db 133 SDIFFORSVPGHD 145

RESULT 16
Q865B8_FELCA PRELIMINARY; PRT; 192 AA.
AC Q865B8;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Interferon gamma inducing factor precursor.
GN Name=fil-18;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kuwahara C., Kawakami K., Kishi M., Mochizuki M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056857; BAC65243.1; -; mRNA.
DR HSSP; Q14116; IJ05.
DR SMR; Q865B8; 36-191.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
KW Signal.
FT SIGNAL 1 35 Potential.
SQ SEQUENCE 192 AA; 22071 MW; 204F32D131588513 CRC64;

Query Match 8.3%; Score 13; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISPKEM 86  
Db 109 LSCENKIISPKEM 121

## RESULT 17

Q9N1P7\_PIG PRELIMINARY; PRT; 192 AA.  
AC Q9N1P7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin-18.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RA MEDLINE=20356335; PubMed=10901174;  
RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;  
RT "Cloning, sequencing, and expression of porcine interleukin-18 in  
RT Escherichia coli."  
RL Mol. Cells 10:343-347 (2000).  
DR EMBL; AF176949; AAF35169.1; -; mRNA.  
DR HSSP; Q14116; 1J0S.  
DR SMR; Q9N1P7; 36-192.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;

Query Match 8.3%; Score 13; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DIIFQFORSVPGHD 110  
Db 133 DIIFQFORSVPGHD 145

## RESULT 18

Q95M33\_FELCA PRELIMINARY; PRT; 192 AA.  
AC Q95M33;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Interferon-gamma inducing factor (IL-18).  
GN Name=IGIF;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Felidae;  
OC Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP Qiao J., Xia X., Yang S.;  
RT "Cloning and sequence analysis of feline IL-18 gene."  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y13923; CAC42918.1; -; mRNA.  
DR EMBL; DQ100372; AAY96319.1; -; mRNA.

DR HSSP; Q14116; 1J0S.  
DR SMR; Q95M33; 36-192.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 8.3%; Score 13; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISPKEM 86  
Db 109 LSCENKIISPKEM 121

## RESULT 19

IL18\_CANFA  
ID IL18 CANFA STANDARD; PRT; 193 AA.  
AC Q9XSR0;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).  
GN Name=IL18; Synonyms=IGIF;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99309818; PubMed=10380699; DOI=10.1007/s002510050532;  
RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;  
RT "Cloning, sequencing, and characterization of dog interleukin-18."  
RL Immunogenetics 49:541-543 (1999).  
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells  
CC and stimulates interferon gamma production in T helper type I  
CC cells (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; Y11133; CAA72015.1; -; mRNA.  
DR SMR; Q9XSR0; 37-192.  
DR Ensembl; ENSCAFG0000013994; Canis familiaris.  
DR GO; GO:0005576; C:extracellular region; TAS.  
DR GO; GO:0005125; F:cytokine activity; TAS.  
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.  
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IEP.  
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.  
DR GO; GO:0042104; P:positive regulation of activated T cell pro. .; ISS.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
KW Cytokine.  
FT PROPEP 1 36 By similarity.  
FT CHAIN 37 193 Interleukin-18.  
SQ SEQUENCE 193 AA; 22037 MW; OD973E586F461F25 CRC64;

Query Match 8.3%; Score 13; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DIIFQFORSVPGHD 110  
Db 133 DIIFQFORSVPGHD 145

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Db      134 DIIFQSVPGHD 146

RESULT 20
IL18_HORSE
ID IL18_HORSE STANDARD; PRT; 193 AA.
AC Q9XSO7;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18; Synonyms=IGIF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type 1
CC cells (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y11131; CAA72013.1; -; mRNA.
DR SNR; Q9XSO7; 37-193.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR KW Cytokine.
DR PROPEP 1 36 By similarity.
DR CHAIN 37 193 Interleukin-18.
DR SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 8.3%; Score 13; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DIIFQSVPGHD 110
Db 134 DIIFQSVPGHD 146

RESULT 21
Q95LE7_CANFA
ID Q95LE7_CANFA PRELIMINARY; PRT; 84 AA.
AC Q95LE7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-18 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Blood;
RX MEDLINE=21589073; PubMed=11730929; DOI=10.1016/S0165-2427(01)00385-3;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantitative analysis of multiple cytokines in canine peripheral
RT blood mononuclear cells by [correction of zby] a single tube RT-PCR.";

Vet. Immunol. Immunopathol. 83:191-202(2001).
DR EMBL; AF327900; AAL28920.1; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR SMR; Q95LE7; 5-83.
DR Ensembl; ENSCAFG00000013994; Canis familiaris.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
FT NON_TER 1 84
FT NON_TER 84 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 6.4%; Score 10; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 IRLNDQVLF 21
Db 16 IRLNDQVLF 25

RESULT 22
Q80Y07_MERUN
ID Q80Y07_MERUN PRELIMINARY; PRT; 195 AA.
AC Q80Y07;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 18.
GN Name=IL18;
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Gerbillinae; Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peritoneum;
RX MEDLINE=22593022; PubMed=12706898; DOI=10.1016/S0378-1119(03)00457-8;
RA Gaucher D., Chadee K.;
RT "Gerbil interleukin-18 and caspase-1: cloning, expression and
RT characterization.";
RL Gene 307:159-166(2003).
DR EMBL; AY095932; AAM34434.1; -; mRNA.
DR HSSP; Q14116; 1J0S.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR SEQUENCE 195 AA; 22172 MW; C6P815317953154D CRC64;

Query Match 5.1%; Score 8; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 NKMQPSS 118
Db 147 NKMQPSS 154

RESULT 23
Q5T9Y7_HUMAN
ID Q5T9Y7_HUMAN PRELIMINARY; PRT; 660 AA.
AC Q5T9Y7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Novel protein (Fragment)
GN Name=RP4-776P7.2; ORFNames=RP4-776P7.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

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OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE.  
 RP Martin S.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RN NUCLEOTIDE SEQUENCE.  
 RP Brown A.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL139345; CAI22956.1; -; Genomic DNA.  
 DR EMBL; AL121993; CAI22736.1; -; Genomic DNA.  
 DR EMBL; AL121993; CAI22956.1; JOINED; Genomic DNA.  
 DR EMBL; AL139345; CAI22736.1; JOINED; Genomic DNA.  
 FT NON\_TER  
 SQ SEQUENCE 660 AA; 74350 MW; AEC06A510AD5D493 CRC64;  
 Query Match 5.1%; Score 8; DB 2; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 137 ILKXDEL 144  
 |||||  
 Db 273 ILKXDEL 280

RESULT 24  
 Q68D55 HUMAN  
 ID Q68D55 HUMAN PRELIMINARY; PRT; 893 AA.  
 AC Q68D55;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein DKFZp686H0726.  
 GN Name=DKFZp686H0726;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE.  
 RP Tissue=Testis;  
 RC The German CDNA Consortium;  
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR749570; CAH18365.1; -; mRNA.  
 DR GO; GO:0005096; F:GTPase activator activity; IEA.  
 DR InterPro; IPR000219; RhoGEF.  
 DR Pfam; PF00621; RhoGEF; 1.  
 DR SMART; SM00325; RhoGEF; 1.  
 DR PROSITE; PS50010; DH.2; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 893 AA; 100316 MW; F65D623C84EBEED CRC64;  
 Query Match 5.1%; Score 8; DB 2; Length 893;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 136 LILKXDEL 143  
 |||||  
 Db 794 LILKXDEL 801

RESULT 25  
 ARHGA HUMAN  
 ID ARHGA HUMAN STANDARD; PRT; 1139 AA.  
 AC O15013; O14665; Q8IWD9; Q8IY77;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Rho guanine nucleotide exchange factor 10.

GN Name=ARHGEF10; Synonyms=KIAA0294;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RP Tissue=Brain;  
 RC MEDLINE=97349984; PubMed=9205841;  
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. VII.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 4:141-150(1997).  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).  
 RP Tissue=Ductum, and Prostate;  
 RC MEDLINE=22158633; PubMed=12168954;  
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
 RT curation of 330 KIAA cDNA clones."  
 RL DNA Res. 9:99-106(2002).  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).  
 RP Tissue=Ductum, and Prostate;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN NUCLEOTIDE SEQUENCE OF 123-1139 (ISOFORM 4).  
 RP Tissue=Brain;  
 RC PubMed=9314494;  
 RA Ranta S., Lehesjoki A.-E., de Fatima Bonaldo M., Knowles J.A.,  
 RA Hirvasniemi A., Ross B., de Jong P.J., Soares M.B., de la Chapelle A.,  
 RA Gilliam T.C.;  
 RT "High-resolution mapping and transcript identification at the  
 RT progressive epilepsy with mental retardation locus on chromosome 8p."  
 RL Genome Res. 7:887-896(1997).  
 RN FUNCTION, AND VARIANT SMCV ILE-127.  
 RP MEDLINE=22870321; PubMed=14508709; DOI=10.1086/378159;  
 RA Verhoeven K., De Jonghe P., Van de Putte T., Nelis E., Zwijsen A.,  
 RA Verpoorten N., De Vriendt E., Jacobs A., Van Gerwen V., Francis A.,  
 RA Ceuterick C., Huybroeck D., Timmerman V.;  
 RT "Slowed conduction and thin myelination of peripheral nerves  
 RT associated with mutant rho guanine-nucleotide exchange factor 10."  
 RL Am. J. Hum. Genet. 73:926-932(2003).  
 CC -!- FUNCTION: May play a role in developmental myelination of  
 CC peripheral nerves.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=O15013-1; Sequence=Displayed;  
 CC Name=2;

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CC CC IsoId=O15013-2; Sequence=VSP_010700, VSP_010701, VSP_010705,
CC CC VSP_010706;
CC CC Note=No experimental confirmation available;
CC CC Name=3;
CC CC IsoId=O15013-3; Sequence=VSP_010701, VSP_010702, VSP_010703;
CC CC Note=No experimental confirmation available;
CC CC Name=4;
CC CC IsoId=O15013-4; Sequence=VSP_010704;
CC CC Note=No experimental confirmation available;
CC CC -!- DISASE: Defects in ARHGEF10 are the cause of slowed nerve
CC CC conduction velocity (SNCV) [MIM:608236]. Affected individuals
CC CC present a reduction in nerve conduction velocities without any
CC CC clinical signs of peripheral or central nervous system
CC CC dysfunction. SNCV inheritance is autosomal dominant.
CC CC -!- SIMILARITY: Contains 1 DH (DBL-homology) domain.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC CC EMBL; AB002292; BAA20754.2; ALT_INIT; mRNA.
CC CC EMBL; BC036809; AAH36809.1; -; mRNA.
CC CC EMBL; BC040474; AAH40474.1; -; mRNA.
CC CC EMBL; AF009205; AAH71662.1; -; mRNA.
CC CC PIR; T03307; T03307.
CC CC DR Ensembl; ENSG00000104728; Homo sapiens.
CC CC DR HGNC; HGNC:14103; ARHGEF10.
CC CC DR MIM; 608136; -.
CC CC DR MIM; 608236; -.
CC CC DR InterPro; IPR001331; GDS_CDC24.
CC CC DR InterPro; IPR000219; RhoGEF.
CC CC DR Pfam; PF00621; RhoGEF; 1.
CC CC DR SMART; SM00325; RhoGEF; 1.
CC CC DR PROSITE; PS00741; DH_1; FALSE_NEG.
CC CC DR PROSITE; PS50010; DH_2; 1.
CC CC KW Alternative splicing; Coiled coil; Disease mutation;
CC CC Guanine-nucleotide releasing factor.
CC CC FT DOMAIN 191 378
CC CC FT COILED 75 95 Potential.
CC CC FT COILED 104 124 Potential.
CC CC FT COILED 360 394 Potential.
CC CC FT COMPIAS 1041 1074 Ser-rich.
CC CC FT VARSPPLIC 1 21 MENPEEAIVDDVPRENSDSEP -> MHS (in isoform
CC CC 2).
CC CC FT FTId=VSP_010700.
CC CC FT Missing (in isoform 2 and isoform 3).
CC CC FT FTId=VSP_010701.
CC CC FT LSSGSRYLRSDDMIETVYNDGRGEIVKTKERRVFMNDVL
CC CC FT MCATV -> VERGFLQLYSKIIFALC (in isoform
CC CC 3).
CC CC FT FTId=VSP_010702.
CC CC FT Missing (in isoform 3).
CC CC FT FTId=VSP_010703.
CC CC FT Missing (in isoform 4).
CC CC FT FTId=VSP_010704.
CC CC FT IGSCTHQMGQIAIVSFQNSPKVIECNVESRILCMLYPVV
CC CC FT EEKRRFPAPPDPETPAVRASDVPTICVGTTEG -> VRCV
CC CC FT YLVLVGVHRESTFMVGMWRD (in isoform 2).
CC CC FT FTId=VSP_010705.
CC CC FT Missing (in isoform 2).
CC CC FT FTId=VSP_010706.
CC CC FT T -> I (in SNCV).
CC CC FT FTId=VAR_019118.
CC CC FT D -> V (in Ref. 3; AAH40474).
CC CC FT CONFLICT 270 270 Missing (in Ref. 3; AAH36809).
CC CC FT CONFLICT 627 627 Missing (in Ref. 4).
CC CC FT CONFLICT 794 794 T -> S (in Ref. 4).
CC CC FT CONFLICT 816 816 S -> T (in Ref. 4).
CC CC FT SEQUENCE 1139 AA; 127119 MW; 8F85F21F327F0CE7 CRC64;
CC CC
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 136 LILKXEDE 143
Db 565 LILKXEDE 572

Search completed: January 30, 2006, 08:58:07
Job time : 171 secs
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Query Match 5.1%; Score 8; DB 1; Length 1139;  
Best Local Similarity 100.0%; Pred. No. 35;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:59:06 ; Search time 32 Seconds  
(without alignments)  
53.130 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 157  
Sequence: 1 YFGKLEKLSVIRLNQDVL.....LKKEDELGDRSIMFTVQNEED 157

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 75621 seqs, 10829074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: listing first 100 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	53.5	157	6	US-10-401-386B-64
2	84	53.5	157	6	US-10-401-386B-70
3	84	53.5	157	6	US-10-401-386B-76
4	84	53.5	157	6	US-10-401-386B-78
5	84	53.5	157	6	US-10-401-386B-80
6	81	51.6	157	6	US-10-401-386B-68
7	55	35.0	157	6	US-10-401-386B-66
8	54	34.4	157	6	US-10-401-386B-72
9	58	5.1	556	7	US-11-024-959-470
10	7	4.5	366	7	US-11-024-959-470
11	6	3.8	16	7	US-11-106-932-56
12	6	3.8	31	7	US-11-106-932-4
13	6	3.8	151	6	US-10-793-626-2696
14	6	3.8	199	7	US-11-113-424-44
15	6	3.8	209	7	US-11-055-822-88
16	6	3.8	209	7	US-11-055-822-90
17	6	3.8	256	6	US-10-877-346-74
18	6	3.8	281	6	US-10-131-826A-372
19	6	3.8	310	6	US-10-063-703-140
20	6	3.8	310	7	US-11-102-240-140
21	6	3.8	318	7	US-11-109-156-15
22	6	3.8	318	7	US-11-111-239-2
23	6	3.8	333	7	US-11-004-789-2
24	6	3.8	334	7	US-11-111-239-4
25	6	3.8	334	7	US-11-127-817-14
					Sequence 64, Appl
					Sequence 70, Appl
					Sequence 76, Appl
					Sequence 78, Appl
					Sequence 80, Appl
					Sequence 88, Appl
					Sequence 86, Appl
					Sequence 302, Appl
					Sequence 470, Appl
					Sequence 56, Appl
					Sequence 4, Appl
					Sequence 296, Appl
					Sequence 44, Appl
					Sequence 88, Appl
					Sequence 90, Appl
					Sequence 74, Appl
					Sequence 140, Appl
					Sequence 15, Appl
					Sequence 2, Appl
					Sequence 4, Appl
					Sequence 14, Appl

26	6	3.8	334	7	US-11-127-877-69	Sequence 69, Appl
27	6	3.8	338	7	US-11-151-601-18	Sequence 18, Appl
28	6	3.8	344	6	US-10-467-657-2616	Sequence 2616, Ap
29	6	3.8	344	6	US-10-995-561-740	Sequence 740, App
30	6	3.8	344	6	US-10-995-561-744	Sequence 744, App
31	6	3.8	389	6	US-10-821-234-1401	Sequence 1401, Ap
32	6	3.8	391	6	US-10-995-561-739	Sequence 739, App
33	6	3.8	409	6	US-10-517-939-292	Sequence 292, App
34	6	3.8	432	6	US-10-995-561-738	Sequence 738, App
35	6	3.8	436	6	US-10-131-826A-404	Sequence 404, App
36	6	3.8	445	6	US-10-995-561-746	Sequence 746, App
37	6	3.8	452	6	US-10-793-626-1834	Sequence 1834, Ap
38	6	3.8	457	6	US-10-995-561-741	Sequence 741, App
39	6	3.8	491	6	US-10-995-561-743	Sequence 743, App
40	6	3.8	512	6	US-10-995-561-745	Sequence 745, App
41	6	3.8	615	7	US-11-172-145-6	Sequence 6, Appli
42	6	3.8	617	7	US-11-172-145-8	Sequence 8, Appli
43	6	3.8	651	7	US-11-172-145-10	Sequence 10, Appl
44	6	3.8	655	6	US-10-467-657-3168	Sequence 3168, Ap
45	6	3.8	753	6	US-10-485-517-173	Sequence 173, App
46	6	3.8	1094	6	US-10-517-939-144	Sequence 144, App
47	6	3.8	1104	7	US-11-099-855-11	Sequence 11, Appl
48	6	3.8	1198	6	US-10-453-372-880	Sequence 880, App
49	6	3.8	1450	6	US-10-055-877-48	Sequence 48, Appl
50	6	3.8	1450	6	US-10-453-372-874	Sequence 874, App
51	6	3.8	2551	7	US-11-052-554A-368	Sequence 368, App
52	6	3.8	3568	6	US-10-453-372-194	Sequence 194, App
53	6	3.8	3570	6	US-10-453-372-178	Sequence 178, App
54	6	3.8	3570	6	US-10-453-372-196	Sequence 196, App
55	6	3.8	3570	6	US-10-453-372-198	Sequence 198, App
56	6	3.8	3570	6	US-10-453-372-200	Sequence 200, App
57	6	3.8	3570	6	US-10-453-372-202	Sequence 202, App
58	6	3.8	3570	6	US-10-453-372-204	Sequence 204, App
59	6	3.8	3570	6	US-10-453-372-206	Sequence 206, App
60	5	3.2	8	7	US-11-045-024-2504	Sequence 2504, Ap
61	5	3.2	8	7	US-11-045-024-5616	Sequence 5616, Ap
62	5	3.2	9	7	US-11-136-079-582	Sequence 582, App
63	5	3.2	10	6	US-10-880-238-30	Sequence 30, Appl
64	5	3.2	10	6	US-10-880-238-33	Sequence 33, Appl
65	5	3.2	13	6	US-10-509-917-3	Sequence 3, Appli
66	5	3.2	15	6	US-10-889-197-9	Sequence 9, Appli
67	5	3.2	15	7	US-11-022-562-22	Sequence 22, Appl
68	5	3.2	15	7	US-11-022-562-23	Sequence 23, Appl
69	5	3.2	17	6	US-10-989-226-2	Sequence 2, Appli
70	5	3.2	17	6	US-10-929-988-338	Sequence 338, App
71	5	3.2	17	7	US-10-834-397-233	Sequence 29, Appl
72	5	3.2	17	7	US-11-066-967-29	Sequence 13, Appl
73	5	3.2	18	6	US-10-889-197-13	Sequence 13, Appl
74	5	3.2	18	6	US-10-929-988-339	Sequence 339, App
75	5	3.2	18	6	US-10-929-988-340	Sequence 340, App
76	5	3.2	18	6	US-10-929-988-475	Sequence 475, App
77	5	3.2	18	7	US-11-033-039-998	Sequence 998, App
78	5	3.2	20	7	US-11-022-562-276	Sequence 276, App
79	5	3.2	20	7	US-11-022-562-277	Sequence 277, App
80	5	3.2	20	7	US-11-022-562-278	Sequence 278, App
81	5	3.2	20	7	US-11-022-562-279	Sequence 279, App
82	5	3.2	20	7	US-11-041-893-190	Sequence 190, App
83	5	3.2	22	7	US-11-041-893-197	Sequence 197, App
84	5	3.2	23	7	US-11-041-893-195	Sequence 195, App
85	5	3.2	27	7	US-11-031-851-5	Sequence 5, Appli
86	5	3.2	27	7	US-11-031-851-7	Sequence 7, Appli
87	5	3.2	27	7	US-11-031-851-19	Sequence 19, Appl
88	5	3.2	27	7	US-11-031-851-21	Sequence 21, Appl
89	5	3.2	28	7	US-11-031-851-11	Sequence 11, Appl
90	5	3.2	28	7	US-11-031-851-20	Sequence 20, Appl
91	5	3.2	29	7	US-11-031-851-12	Sequence 12, Appl
92	5	3.2	29	7	US-11-031-851-13	Sequence 13, Appl
93	5	3.2	29	7	US-11-031-851-14	Sequence 14, Appl
94	5	3.2	29	7	US-11-031-851-15	Sequence 15, Appl
95	5	3.2	29	7	US-11-031-851-23	Sequence 23, Appl
96	5	3.2	30	6	US-10-467-657-2370	Sequence 2370, Ap
97	5	3.2	37	6	US-10-957-351-24	Sequence 24, Appl
98	5	3.2	37	6	US-10-957-351-139	Sequence 139, App

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99 5 3.2 43 6 US-10-957-887B-230 Sequence 230, App
100 5 3.2 47 6 US-10-467-657-4844 Sequence 4844, Ap

ALIGNMENTS

RESULT 1
US-10-401-386B-64
; Sequence 64, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-64

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Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
Db |
QY 134 FKILKKEDELGDRSIMFTVQNEED 157
Db |

RESULT 2
US-10-401-386B-70
; Sequence 70, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-70

Query Match 53.5%; Score 84; DB 6; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
Db |
QY 134 FKILKKEDELGDRSIMFTVQNEED 157
Db |

RESULT 3
US-10-401-386B-76
; Sequence 76, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-76

Query Match 53.5%; Score 84; DB 6; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
Db |
QY 134 FKILKKEDELGDRSIMFTVQNEED 157
Db |

RESULT 4
US-10-401-386B-78
; Sequence 78, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
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; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-78

Query Match
Best Local Similarity 100.0%; Score 84; DB 6; Length 157;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||
74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Qy 134 FKLLKKEDELGDRSIMFTVQNE 157
Db |||||
134 FKLLKKEDELGDRSIMFTVQNE 157

RESULT 5
US-10-401-386B-80
; Sequence 80, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-80

Query Match
Best Local Similarity 100.0%; Score 84; DB 6; Length 157;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Db |||||
74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Qy 134 FKLLKKEDELGDRSIMFTVQNE 157
Db |||||
134 FKLLKKEDELGDRSIMFTVQNE 157

RESULT 6
US-10-401-386B-68
; Sequence 68, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
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; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-68

Query Match
Best Local Similarity 100.0%; Score 81; DB 6; Length 157;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Db |||||
74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMQFESSSYEGYFLACEKERDL 133
Qy 134 FKLLKKEDELGDRSIMFTVQ 154
Db |||||
134 FKLLKKEDELGDRSIMFTVQ 154

RESULT 7
US-10-401-386B-66
; Sequence 66, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-66

Query Match
Best Local Similarity 100.0%; Score 55; DB 6; Length 157;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 QVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSOPRGMVATISVKCEKIS 72
Db |||||
18 QVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSOPRGMVATISVKCEKIS 72

RESULT 8
US-10-401-386B-72
```

```
; Sequence 72, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Brangan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen J McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-401-386B-72

Query Match      34.4%; Score 54; DB 6; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.2e-48;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 IISFKEMNPPDNIKDTKSDIIFQRSVPGHDKNQFESSYEGYFLACEKRD 133
DB 80 IISFKEMNPPDNIKDTKSDIIFQRSVPGHDKNQFESSYEGYFLACEKRD 133

RESULT 9
US-11-124-368A-303
; Sequence 303, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-303

Query Match      5.1%; Score 8; DB 7; Length 556;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 ILKKEDEL 144
DB 428 ILKKEDEL 435

RESULT 10
US-11-024-959-470
; Sequence 470, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-470

Query Match      4.5%; Score 7; DB 7; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 KLILKE 141
DB 316 KLILKE 322

RESULT 11
US-11-106-932-56
; Sequence 56, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC MARKERS FOR CANCER, ORGAN
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-56

Query Match      3.8%; Score 6; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 EKERDL 133
DB 8 EKERDL 13

RESULT 12
US-11-106-932-4
; Sequence 4, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC MARKERS FOR CANCER, ORGAN
```

```
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-4

Query Match          3.8%; Score 6; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 128 EKERDL 133
Db 23 EKERDL 28
|||||

RESULT 13
US-10-793-626-2696
; Sequence 2696, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2696
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2696

Query Match          3.8%; Score 6; DB 6; Length 151;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 TIFIIS 50
Db 35 TIFIIS 40
|||||

RESULT 14
US-11-113-424-44
; Sequence 44, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 88
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-88

Query Match          3.8%; Score 6; DB 7; Length 209;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 SVFGHD 110
```

```
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-44

Query Match          3.8%; Score 6; DB 7; Length 199;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 GDRSIM 150
Db 144 GDRSIM 149
|||||

RESULT 15
US-11-055-822-88
; Sequence 88, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 88
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-88

Query Match          3.8%; Score 6; DB 7; Length 209;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 SVFGHD 110
```

Db 130 SVPGHD 135  
|||||

## RESULT 16

US-11-055-822-90  
; Sequence 90, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Krogger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS  
; FILE REFERENCE: BGI-121PCPN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: 60/148,613  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/187,970  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: DE 19930476.9  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931415.2  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931419.5  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931420.9  
; PRIOR FILING DATE: 1999-07-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1158  
; SEQ ID NO 90  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-055-822-90

Query Match 3.8%; Score 6; DB 7; Length 209;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 SVPGHD 110  
Db 130 SVPGHD 135  
|||||

## RESULT 17

US-10-877-346-74  
; Sequence 74, Application US/10877346  
; Publication No. US20060014153A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: MacDougall, John R  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Leach, Martin D  
; APPLICANT: Shinkets, Richard A  
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-124  
; CURRENT APPLICATION NUMBER: US/10/877,346  
; CURRENT FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US/09/964,956  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,631  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,633  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,808  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,064  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,065  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,066  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,135  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/237,434  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/238,321  
; PRIOR FILING DATE: 2000-10-05  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 74  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase  
; OTHER INFORMATION: domain Consensus Sequence  
US-10-877-346-74

Query Match 3.8%; Score 6; DB 6; Length 256;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 ESSSYE 121  
Db 149 ESSSYE 154  
|||||

## RESULT 18

US-10-131-826A-372  
; Sequence 372, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C128  
CURRENT APPLICATION NUMBER: US/10/131,826A  
CURRENT FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 372  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-131-826A-372

Query Match 3.8%; Score 6; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 145 GDRSIM 150  
DB 226 GDRSIM 231

RESULT 19  
US-10-063-703-140  
Sequence 140, Application US/10063703  
Publication No. US20060008901A1  
GENERAL INFORMATION:  
APPLICANT: Baton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,703  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 140  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-703-140

Query Match 3.8%; Score 6; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 VIRNLN 16  
DB 11 VIRNLN 16

Db 133 VIRNLN 138  
RESULT 20  
US-11-102-240-140  
Sequence 140, Application US/11102240  
Publication No. US20050260647A1  
GENERAL INFORMATION:  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES-  
SION  
FILE REFERENCE: P3230R1C106C  
CURRENT APPLICATION NUMBER: US/11/102,240  
CURRENT FILING DATE: 2005-04-08  
PRIOR APPLICATION NUMBER: 10/063662  
PRIOR FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: 10/006867  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: 60/170262  
PRIOR FILING DATE: 199-12-09  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 140  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-102-240-140

Query Match 3.8%; Score 6; DB 7; Length 310;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 VIRNLN 16  
DB 133 VIRNLN 138

RESULT 21  
US-11-109-156-15  
Sequence 15, Application US/11109156  
Publication No. US20050250144A1  
GENERAL INFORMATION:  
APPLICANT: Toshio Ota  
APPLICANT: Takao Isogai  
APPLICANT: Tetsuo Nishikawa  
APPLICANT: Koji Hayashi  
APPLICANT: Kaoru Otsuka  
APPLICANT: Jun-ichi Yamamoto  
APPLICANT: Shizuko Ishii  
APPLICANT: Tomoyasu Sugiyama  
APPLICANT: Ai Wakamatsu  
APPLICANT: Keiichi Nagai  
APPLICANT: Tetsuji Otsuki  
APPLICANT: Shin-ichi Funahashi  
APPLICANT: Chiaki Senoo  
APPLICANT: Jun-ichi Nezu  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN  
PHOSPHATASE  
FILE REFERENCE: 06501-099002  
CURRENT APPLICATION NUMBER: US/11/109,156  
CURRENT FILING DATE: 2005-04-19  
PRIOR APPLICATION NUMBER: US/10/060,065  
PRIOR FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: PCT/JP00/05061  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/159,590  
PRIOR FILING DATE: 1999-10-18  
PRIOR APPLICATION NUMBER: US 60/183,322





;  
; FILING DATE: 21-Apr-2005  
; CLASSIFICATION: <Unknown>  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/761,569  
; FILING DATE: 16-Jan-2001  
; APPLICATION NUMBER: 09/057,009  
; FILING DATE: 1998-04-07  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fasse, J. Peter  
; REGISTRATION NUMBER: 32,983  
; REFERENCE/DOCKET NUMBER: 07917/010001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
;  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 334 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: Not Relevant  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-11-111-239-4

Query Match 3.8%; Score 6; DB 7; Length 334;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 SKLSVI 12  
Db 171 SKLSVI 176

RESULT 25  
US-11-127-817-14  
; Sequence 14, Application US/11127817  
; Publication No. US20050287519A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Methods, Compositions And Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-D USA  
; CURRENT APPLICATION NUMBER: US/11/127,817  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 534  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-127-817-14

Query Match 3.8%; Score 6; DB 7; Length 334;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 SKLSVI 12  
Db 171 SKLSVI 176

Search completed: January 30, 2006, 09:10:33  
Job time : 32 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:42:04 : Search time 134 Seconds  
 (without alignments)  
 514.795 Million cell updates/sec

Title: US-09-716-356A-6  
 Perfect score: 157  
 Sequence: 1 YFGKLESLVIRNLNDQVL.....LKKEDELGDRSMFTVQNEED 157

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A Geneseq 21.\*  
 1: geneseqp1990s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	99.4	157	2	Aar99564 Human int
2	156	99.4	157	2	Aar99558 Human mat
3	156	99.4	157	2	Aaw15701 Interfero
4	156	99.4	157	2	Aaw24258 Human pro
5	156	99.4	157	2	Aaw63810 Human IL-
6	156	99.4	157	2	Aaw52176 Interfero
7	156	99.4	157	2	Aaw77158 Human int
8	156	99.4	157	2	Aaw37741 IFN-gamma
9	156	99.4	157	2	Aay39799 Interleuk
10	156	99.4	157	3	Aay53904 Sequence
11	156	99.4	157	3	Aay44597 Human int
12	156	99.4	157	4	Aab82408 Human int
13	156	99.4	193	2	Aar99560 Human int
14	156	99.4	193	2	AAW52172 Interfero
15	156	99.4	193	2	AAW52172 Interfero
16	156	99.4	193	2	AAW37740 Interfero
17	156	99.4	193	3	AAW53908 Amino aci
18	156	99.4	193	4	AAW82409 Human int
19	156	99.4	193	8	ADL24278 Human IL-
20	84	53.5	157	2	AAW77084 Human int
21	84	53.5	157	2	AAW77077 Human int
22	84	53.5	157	2	AAW77083 Human int
23	84	53.5	157	2	AAW48961 Mutant hu
24	84	53.5	157	2	AAW48962 Mutant hu

25	84	53.5	157	3	AAW57570 Human int
26	84	53.5	157	4	AAG65351 Human int
27	84	53.5	157	4	AAG65294 Human int
28	84	53.5	157	4	AAE06661 Human int
29	84	53.5	157	5	ABW04389 Human IL-
30	84	53.5	157	5	AAE17134 Human IL-
31	84	53.5	157	5	AAE16954 Human act
32	84	53.5	157	6	ABG73364 Human mat
33	84	53.5	157	6	ABG73365 Human mat
34	84	53.5	157	6	ABG73363 Human mat
35	84	53.5	157	6	ABG73367 Human mat
36	84	53.5	157	6	ABG73359 Human wil
37	84	53.5	157	6	ADA50616 Human mat
38	84	53.5	157	6	ADA50622 Human mat
39	84	53.5	157	6	ADA50610 Human mat
40	84	53.5	157	6	ABR83396 Human int
41	84	53.5	157	6	ABR83405 Human int
42	84	53.5	157	6	ABR83406 Human int
43	84	53.5	157	6	ABR83407 Human int
44	84	53.5	157	6	ABR83404 Human int
45	84	53.5	157	6	ABR83372 Human int
46	84	53.5	157	6	ABR83402 Human int
47	84	53.5	157	6	ABR83399 Human int
48	84	53.5	157	6	ABR83401 Human int
49	84	53.5	157	6	ABR83403 Human int
50	84	53.5	157	6	ABR83394 Human int
51	84	53.5	157	6	ABR83397 Human int
52	84	53.5	157	6	ABR83395 Human int
53	84	53.5	157	6	ABR83398 Human int
54	84	53.5	157	7	AAE39507 Human mat
55	84	53.5	157	7	ADW06775 Human ant
56	84	53.5	157	8	ADH54826 Human int
57	84	53.5	157	8	ADL24279 Human IL-
58	84	53.5	157	8	ADN35070 Human IL-
59	84	53.5	157	8	ADS73677 Human int
60	84	53.5	157	8	ADU06896 Human int
61	84	53.5	157	8	ADU06893 Human int
62	84	53.5	157	8	ADU06897 Human int
63	84	53.5	157	8	ADU49648 Human int
64	84	53.5	157	8	ADU49654 Human IL-
65	84	53.5	157	8	ADU49658 Human IL-
66	84	53.5	157	8	ADU49642 Human int
67	84	53.5	157	8	ADU49656 Human IL-
68	84	53.5	157	9	ADV90268 Protease
69	84	53.5	157	9	ADY86605 Human rec
70	84	53.5	157	9	ADZ77759 Human int
71	84	53.5	157	9	ADZ77756 Human int
72	84	53.5	157	9	AE93714 Human mut
73	84	53.5	157	9	AE93702 Human wil
74	84	53.5	158	3	AAW85167 Human int
75	84	53.5	158	8	ADJ88309 Human int
76	84	53.5	158	8	ADJ88309 Human int
77	84	53.5	177	6	ADA50614 Mature co
78	84	53.5	180	2	AAW48959 Wild-type
79	84	53.5	181	3	AAW23797 Human int
80	84	53.5	193	2	AAW22047 Interfero
81	84	53.5	193	2	AAW46592 Amino aci
82	84	53.5	193	4	AAW30541 A human I
83	84	53.5	193	4	AAW63830 Amino aci
84	84	53.5	193	5	AAE16953 Human pre
85	84	53.5	193	6	ABG73366 Human pre
86	84	53.5	193	6	ABG73360 Human pre
87	84	53.5	193	6	ABG73361 Human pre
88	84	53.5	193	6	ABG73362 Human pre
89	84	53.5	193	7	AAE39505 Amino aci
90	84	53.5	193	8	ADN41835 Amino aci
91	84	53.5	193	8	ADP12432 Protein e
92	84	53.5	193	8	ADP64786 Human int
93	84	53.5	193	9	ADZ51271 Amino aci
94	84	53.5	193	9	ADZ70835 Human int
95	84	53.5	193	9	ABW28907 Human int
96	84	53.5	203	8	ADU06895 Human int
97	84	53.5	233	5	AAE16959 Ubiquitin

98 84 53.5 325 9 ADY22168 Human IL-  
99 84 53.5 325 9 ADY22167 Human IL-  
100 84 53.5 361 9 ADY22165 Human IL-

## ALIGNMENTS

RESULT 1  
AAR99564  
ID AAR99564 standard; protein; 157 AA.  
XX  
AC AAR99564;  
XX  
XX 29-SEP-1996 (first entry)  
XX  
DE Human interferon-gamma inducer protein.  
XX  
KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;  
KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;  
KW therapy; cancer.  
XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Misc-difference 73  
FT /label= Ile, Thr  
XX  
XX EP712931-A2.  
XX  
PD 22-MAY-1996.  
XX  
XX 10-NOV-1995; 95EP-00308055.  
XX  
XX 15-NOV-1994; 94JP-00304203.  
XX  
PR 23-FEB-1995; 95JP-00058240.  
XX  
PR 10-MAR-1995; 95JP-00078357.  
XX  
PR 18-SEP-1995; 95JP-00262062.  
XX  
PR 29-SEP-1995; 95JP-00274988.  
XX

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
XX Ushio S, Torigoe K, Tanimoto T, Okamura H, Kunikata T;  
PI Taniguchi M, Kohno K, Fukuda S, Kurimoto M;  
XX  
XX WPI; 1996-252837/26.  
DR N-PSDB; AAT32411.  
XX  
XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful to  
PT treat and prevent, e.g. viral disease, malignancies and immune disorders.  
XX  
XX Example B-1-1; Page 28; 48pp; English.

XX A novel human protein (AAR99564) that induces interferon-gamma (IFN-  
CC gamma) prodn. by immunocompetent cells is the product of a phage cDNA  
CC clone (AAT32411) derived from a human liver library. PCR amplification of  
CC the cDNA (see also AAT32409-10) and expression in Escherichia coli XL-1  
CC Blue MRF-Kan allowed prodn. of recombinant inducer protein. This was used  
CC to construct hybridoma H-1, which produced anti-IFN-gamma inducer protein  
CC monoclonal antibody H-1mab, useful in the detection and purification of  
CC the inducer protein (see also AAR99558)

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 2.1e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKNQFESSY 120

DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKNQFESSY 120  
QY 121 EGYFLACCKERDLFKILIKKEDELGDRSMTFTVQNEED 157  
DB 121 EGYFLACCKERDLFKILIKKEDELGDRSMTFTVQNEED 157

RESULT 2  
AAR99558

ID AAR99558 standard; protein; 157 AA.

XX

AC AAR99558;

XX

DT 29-SEP-1996 (first entry)

XX

DE Human mature interferon-gamma inducer protein.

XX

KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;

KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;

KW therapy; cancer.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 73

FT /label= Ile, Thr

XX

PN EP712931-A2.

XX

PD 22-MAY-1996.

XX

PF 10-NOV-1995; 95EP-00308055.

XX

PR 15-NOV-1994; 94JP-00304203.

XX

PR 23-FEB-1995; 95JP-00058240.

XX

PR 10-MAR-1995; 95JP-00078357.

XX

PR 18-SEP-1995; 95JP-00262062.

XX

PR 29-SEP-1995; 95JP-00274988.

XX

PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX

PI Ushio S, Torigoe K, Tanimoto T, Okamura H, Kunikata T;

PI Taniguchi M, Kohno K, Fukuda S, Kurimoto M;

XX

XX WPI; 1996-252837/26.

DR

DR N-PSDB; AAT32402.

XX

XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful to

PT treat and prevent, e.g. viral disease, malignancies and immune disorders.

XX

PS Claim 1; Page 40; 48pp; English.

XX

CC A novel human protein (AAR99558) induces interferon-gamma (IFN-gamma)

CC prodn. by immunocompetent cells. It enhances the cytotoxicity of killer

CC cells and/or induces the formation of killer cells (e.g. NK cells,

CC lymphokine-activating killer (LAK) cells, and cytotoxic T-cells).

CC Recombinant IFN-gamma inducer protein can be produced in high yields

CC using host cells, esp. Escherichia coli, transformed with a vector

CC carrying the encoding cDNA (AAT32402). It is useful as an antiviral,

CC antitumor, antibacterial, immunoregulatory and blood platelet enhancing

CC agent, and can be used in adoptive immunotherapy. It is also used to

XX raise monoclonal antibodies. A full-length sequence is given in AAR99560

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 2.1e-162;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKNQFESSY 120

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSRVPGHDKMQFESSY 120  
 DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSRVPGHDKMQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 3  
 AAW15701  
 ID AAW15701 standard; protein; 157 AA.  
 XX  
 AC AAW15701;  
 DT 26-JAN-1998 (first entry)  
 XX  
 DE Interferon-gamma inducer protein.  
 XX  
 KW Interferon-gamma, IFN-gamma; antiviral; antioncotic; radiotherapy;  
 immunoregulatory; antitumour agent; chemotherapy; leukopaemia;  
 KW thrombocytopaenia; immunocompetent cell; asthma; hayfever; rheumatism;  
 KW interleukin; killer cell.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 73  
 FT /label= Ile, Thr  
 XX  
 PN EP767178-Al.  
 XX  
 PD 09-APR-1997.  
 XX  
 XX 26-SEP-1996; 96EP-00306997.  
 XX  
 PR 26-SEP-1995; 95JP-00270725.  
 PR 29-FEB-1996; 96JP-00067434.  
 PR 20-SEP-1996; 96JP-00269105.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 PI Akita K, Nukada Y, Fujii M, Tanimoto T, Kurimoto M;  
 XX  
 DR WPI; 1997-205381/19.  
 XX  
 PT Human protein that induces interferon-gamma prodn. in immuno:competent  
 PT cells - useful for adoptive immuno:therapy of tumours and as  
 PT antimicrobial agent etc.  
 XX  
 PS Claim 8; Page 20; 26pp; English.  
 XX  
 CC The present sequence represents a novel protein from human cells, which  
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.  
 CC This protein enhances cytotoxicity of killer cells and induces their  
 CC formation. It is used as an antioncotic agent for antitumour  
 CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,  
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,  
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also  
 CC used to treat leukopaemia and thrombocytopaenia associated with  
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in  
 CC antitumour immunotherapy, this novel protein significantly improves the  
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of IL  
 CC -2 alone, either when administered to the patient (before administration  
 CC of IL-2) or by addition to the medium in which cells (intended for return  
 CC to the patient) are being grown

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 2.le-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSRVPGHDKMQFESSY 120  
 DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSRVPGHDKMQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4  
 AAW24258  
 ID AAW24258 standard; protein; 157 AA.  
 XX  
 AC AAW24258;  
 XX  
 DT 15-OCT-1997 (first entry)  
 XX  
 DE Human protein for induction of interferon-gamma.  
 XX  
 KW Interferon-gamma; immunocompetent cell; malignant tumour; viral disease;  
 KW bacterial infection; immune disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 73  
 FT /note= "Encoded by AYT"  
 XX  
 PN JP09157180-A.  
 XX  
 PD 17-JUN-1997.  
 XX  
 PF 24-JAN-1996; 96JP-00028722.  
 XX  
 PR 10-MAR-1995; 95JP-00078357.  
 PR 29-SEP-1995; 95JP-00274988.  
 PR 04-OCT-1995; 95JP-00279906.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 DR WPI; 1997-369391/34.  
 DR N-PSDB; AAT80209.  
 XX  
 PT A drug containing a polypeptide which induces interferon-gamma - useful  
 PT for treating e.g. malignant tumours, viral, bacterial or immune diseases.  
 XX  
 PS Claim 1; Page 9; 12pp; Japanese.  
 XX  
 CC This sequence represents a protein which induces interferon-gamma  
 CC production in immunocompetent cells. This protein may be used as the  
 CC major component in a drug for the prevention and treatment of e.g.  
 CC malignant tumours, viral diseases, bacterial infections and immune  
 CC diseases  
 XX  
 SQ Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 2.le-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60  
 DB 1 YFGKLESKLSVIRNLNDQVLFIIDQGNRPLFEDMTSDCRDNAPRTIIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSRVPGHDKMQFESSY 120  
 DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQSRVPGHDKMQFESSY 120



Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 7

AAW77158  
ID AAW77158 standard; protein; 157 AA.

XX AC AAW77158;  
XX DT 26-NOV-1998 (first entry)  
XX DE Human interleukin-18 protein (IL-18).

XX KW Human; interleukin-18 receptor; IL-18R; cytokine; signal transduction;  
XX KW immune system; treatment; autoimmune; allergic disease;  
XX KW immunosuppressant.  
XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT Misc-difference 73  
XX FT /note= "Ile or Thr"

XX PN EP864585-A1.  
XX PD 16-SEP-1998.

XX PF 23-DEC-1997; 97EP-00310517.  
XX PR 12-MAR-1997; 97JP-00074697.

XX PR 28-JUL-1997; 97JP-00215488.  
XX PR 09-OCT-1997; 97JP-00291837.

XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX PI Torigoe K, Okura T, Kurimoto M;

XX DR WPI; 1998-469188/41.  
XX PT Interleukin-18 receptor polypeptide(s) - and corresponding DNA, which  
XX PT peptide compounds are useful for treating auto-immune or allergic  
XX PT diseases.

XX PS Disclosure; Page 41-42; 51pp; English.  
XX CC The present sequence represents a human interleukin-18 (IL-18)

XX CC polypeptide. Interleukin-18 is a type of cytokine which mediates signal  
XX CC transduction in immune systems. The interleukin-18 receptor polypeptide  
XX CC can be used to neutralise interleukin-18 activity or to treat interleukin  
XX CC -18 receptor susceptible diseases, especially to treat autoimmune or  
XX CC allergic diseases or as an immunosuppressant. Conditions which may be  
XX CC treated include e.g. graft or organ rejection, pernicious anaemia,  
XX CC insulin-related diabetes, discoid lupus erythematosus, ulcerative  
XX CC colitis, hyperthyroidism, auto-immune hepatitis, systemic scleroderma,  
XX CC polymyositis, leukopenia, rheumatoid arthritis, HIV infections, asthma,  
XX CC atopic dermatitis, and pollinosis. The products may also be useful in the  
XX CC treatment of septic shock associated with IFN-alpha

XX SQ Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No: 2.1e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFORSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 8

AAW37741  
ID AAW37741 standard; protein; 157 AA.

XX AC AAW37741;  
XX DT 07-JUL-1998 (first entry)  
XX DE IFN-gamma inducing active protein.

XX KW Interferon-gamma inducing precursor peptide; IFN-gamma;  
XX KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;  
XX KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.  
XX OS Mammalia.

XX FH Key Location/Qualifiers  
XX FT Misc-difference 73  
XX FT /label= Ile, Thr

XX PN EP821005-A2.  
XX PD 28-JAN-1998.

XX PF 18-JUL-1997; 97EP-00305376.  
XX PR 25-JUL-1996; 96JP-00213267.

XX PR 31-JAN-1997; 97JP-00031474.  
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Tanimoto T, Kurimoto M;  
XX DR WPI; 1998-088847/09.

XX DR N-PSDB; AAV18906.  
XX PT Conversion of interferon-inducing polypeptide precursor to active  
XX PT polypeptide - comprises use of interferon-1-beta-converting enzyme,  
XX PT useful for, e.g. enhancing cytotoxicity by killer cells.

XX PS Claim 5; Page 15; 18pp; English.  
XX CC This is the amino acid sequence for the interferon-gamma (IFN-gamma)

XX CC inducing active protein which is cleaved to form the active mature  
XX CC protein when it is in contact with interleukin-1-beta-converting enzyme  
XX CC (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma  
XX CC a useful biologically active substance, enhancing cytotoxicity by, and  
XX CC inducing the formation of killer cells. The polypeptide may potentially  
XX CC be used as an antiviral, antitumour and immunopathy agent and as an  
XX CC antiseptic

XX SQ Sequence 157 AA;

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No: 2.1e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRNPRTFIISMVKDSQPRGM 60

```
QY 61 AVTISVCKEIKSLXSCENKIISFKEMNPPDNIKDTSKDIIFFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVCKEIKSLXSCENKIISFKEMNPPDNIKDTSKDIIFFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 9
AAY39799
ID AAY39799 standard; protein; 157 AA.
XX AC AAY39799;
XX DT 29-NOV-1999 (first entry)
XX DE Interleukin-18 receptor protein sequence fragment.
XX KW Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;
XX KW IL-18 receptor sensitive disease; immune reaction; therapy.
XX OS Mammalia.
XX FH Key Location/Qualifiers
XX FT Misc-difference 73
XX FT /note= "unspecified amino acid"
XX JP11240898-A.
XX PN 07-SEP-1999.
XX PD
XX PF 12-MAR-1998; 98JP-00078549.
XX PR 12-MAR-1997; 97JP-00074697.
XX PR 28-JUL-1997; 97JP-00215488.
XX PR 09-OCT-1997; 97JP-00291837.
XX PR 28-DEC-1997; 97JP-00366908.
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX WPI; 1999-555071/47.
XX PT New polypeptide - useful against interleukin-18 receptor sensitive
XX PT diseases.
XX PS Disclosure; Page 37; 41pp; Japanese.
XX CC This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the
XX CC invention. The IL-18R sequences were isolated from human and mouse. The
XX CC sequences can be used in drugs for treating IL-18 receptor sensitive
XX CC disease, especially effective for the relief of rejection accompanied to
XX CC organ transplantation and for the treatment and the prevention of various
XX CC diseases caused by excessive immune reaction.
XX SQ Sequence 157 AA;
Query Match 99.4%; Score 156; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.1e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTPIIISMYKDSQPRGM 60
Db 1 YFGKLSKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTPIIISMYKDSQPRGM 60
QY 61 AVTISVCKEIKSLXSCENKIISFKEMNPPDNIKDTSKDIIFFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVCKEIKSLXSCENKIISFKEMNPPDNIKDTSKDIIFFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
```

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RESULT 10
AAY53904
ID AAY53904 standard; protein; 157 AA.
XX AC AAY53904;
XX DT 13-MAR-2000 (first entry)
XX DE Sequence of a mature protein that induces IFN-gamma production.
XX DE Human; interferon gamma production; IFN-gamma; immunocompetent cell;
XX KW antiviral; immunoregulatory; antigen; mitogen;
XX KW IFN-gamma susceptible disease; antibacterial; antitumour;
XX KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;
XX KW AIDS; bacterial disease; Candidiasis; malaria; solid malignant tumour;
XX KW renal cancer; mycosis fungoides; chronic granulomatous disease;
XX KW blood cell malignant tumour; adult T cell leukaemia;
XX KW chronic myelogenous leukaemia; malignant leukaemia; immune disease;
XX KW allergy; rheumatism.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 73
XX FT /label= Ile, Thr
XX FT /note= "encoded by AYT"
XX EP962531-A2.
XX PN 08-DEC-1999.
XX PD
XX PF 10-NOV-1995; 99EP-00104104.
XX PR 15-NOV-1994; 94JP-00304203.
XX PR 23-FEB-1995; 95JP-00058240.
XX PR 10-MAR-1995; 95JP-00078357.
XX PR 18-SEP-1995; 95JP-00262062.
XX PR 29-SEP-1995; 95JP-00274988.
XX PR 10-NOV-1995; 95EP-00308055.
XX PA (HAYB.) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI Ushio S. Torigoe K. Tanimoto T. Okamura H.;
XX WPI; 2000-064289/06.
XX DR N-P8DB; AA236875.
XX PT Novel polypeptides used in the treatment of interferon-gamma susceptible
XX PT diseases.
XX CC Claim 1; Page 4; 42pp; English.
XX CC The present sequence represents a human protein that induces interferon
XX CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a protein
XX CC which has antiviral, antineoplastic and immunoregulatory activities and is
XX CC produced by immunocompetent cells stimulated with antigens or mitogens.
XX CC The protein of the invention is used to treat IFN-gamma susceptible
XX CC diseases, and also have use as a antiviral agent, antibacterial agent,
XX CC antitumour agent, immunoregulatory agent and blood platelet enhancing
XX CC agent. Diseases which can be treated with the protein include viral
XX CC diseases such as hepatitis, herpes syndrome, condyloma, and AIDS;
XX CC bacterial diseases such as Candidiasis and malaria; solid malignant
XX CC tumours such as renal cancer, mycosis fungoides, and chronic
XX CC granulomatous disease; blood cell malignant tumours such as adult T cell
XX CC leukaemia, chronic myelogenous leukaemia, and malignant leukaemia; and
XX CC immune diseases such as allergy and rheumatism
XX SQ Sequence 157 AA;
Query Match 99.4%; Score 156; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.1e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 11

AA44597  
ID AAY44597 standard; protein; 157 AA.

XX AC AAY44597;

DT 04-APR-2000 (first entry)

XX Human interleukin-18.

DE Human interleukin-18; IL-18; anti-IL-18-antibody; immunopathies;  
KW inflammatory disorder; autoimmune disease; anti-allergic;  
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopenic;  
KW antialgic; antipyretic.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 73  
FT /label= Ile, Thr

XX EP974600-A2.

XX 26-JAN-2000.

XX 24-JUN-1999; 99EP-00304977.

XX 24-JUN-1998; 98JP-00177580.

PR 12-OCT-1998; 98JP-00289044.

PR 22-DEC-1998; 98JP-00365023.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Nishida Y, Okura T, Tanimoto T, Kurimoto M;

XX WPI; 2000-118341/11.

XX New artificially produced peptide for neutralizing biological activity of  
PT interleukin-18, useful for treating and preventing immunopathies,  
PT inflammatory disorders and autoimmune diseases.

XX Example 1; Page 26; 32pp; English.

XX The present sequence is human interleukin-18. This was used to immunise  
CC BALB/c mice to generate hybridomas that produce anti-IL-18 antibodies for  
CC neutralising interleukin-18. This is useful for treating and preventing  
CC immunopathies, inflammatory disorders and autoimmune diseases which are  
CC caused by excessive immunoreaction. The protein has anti-allergic, anti-  
CC inflammatory, immunosuppressive, hematopoietic, leukocytopenic,  
CC antialgic, antipyretic and hepatic-function improving activities

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 2.1e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
|||||

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 12

AAB82408

ID AAB82408 standard; protein; 157 AA.

XX AC AAB82408;

DT 06-AUG-2001 (first entry)

DE Human interleukin-18 mature polypeptide.

XX Interleukin-18; antibody; human; infection; tumour; sarcoma;  
KW autoimmune disease; therapy; diagnosis; detoxification.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 73  
FT /label= Ile, Thr

XX EPI101772-A1.

XX 23-MAY-2001.

XX 15-NOV-2000; 2000EP-00310121.

XX 16-NOV-1999; 99JP-00324860.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.

XX Tohru K, Taniguchi M, Yamauchi H, Kurimoto M;

XX WPI; 2001-368892/39.

XX New antibodies specific to interleukin 18 (IL-18) precursor, useful in  
PT manufacturing a medicament for treating IL-18-related diseases, e.g.  
PT autoimmune disease, or for detecting, eliminating or detoxifying the  
PT precursor.

XX Disclosure; Page 13-14; 27pp; English.

XX The present sequence is that of human interleukin-18 (IL-18) mature  
CC protein. Monoclonal and polyclonal antibodies specific to the human IL-18  
CC precursor propeptide (see AAB82406) are claimed. These are useful in  
CC detection and purification of IL-18 precursor, and in the elimination and  
CC detoxification of the precursor accumulated in vivo. Detection methods  
CC using the antibody are effective in qualitative and quantitative analyses  
CC for the precursor, and also in the correction of imprecise results  
CC obtained from assays using anti-IL-18 antibody, which exhibit cross-  
CC reactivity against the precursor. Pharmaceutical compositions comprising  
CC an antibody specific to the IL-18 precursor can be used to treat viral  
CC infections including AIDS, bacterial infections, solid malignant tumours,  
CC malignant tumours of haemocytes, sarcomas, autoimmune disease,  
CC hepatopathy, pancreatopathy, and diseases of the gallbladder, kidney and  
CC nervous system. Detection methods using the antibody can be used to  
CC diagnose such diseases

XX Sequence 157 AA;

Query Match 99.4%; Score 156; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 2.1e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIIFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120  
DB 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
RESULT 13  
ID AAR99560 standard; protein; 193 AA.  
XX AAR99560;  
XX AC AAR99560;  
XX DT 29-SEP-1996 (first entry)  
XX DE Human interferon-gamma inducer protein.  
XX DE Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;  
KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;  
KW therapy; cancer.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Peptide 1..36  
FT Protein /label= Leader\_peptide  
FT FT 37..193  
FT FT /label= Mat\_protein  
FT FT Misc-difference 109  
FT FT /label= Ile, Thr  
XX EP712931-A2.  
XX PD 22-MAY-1996.  
XX PF 10-NOV-1995; 95EP-00308055.  
XX PR 15-NOV-1994; 94JP-00304203.  
XX PR 23-FEB-1995; 95JP-00058240.  
XX PR 10-MAR-1995; 95JP-00078357.  
XX PR 18-SEP-1995; 95JP-00262062.  
XX PR 29-SEP-1995; 95JP-00274988.  
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX PA Ushio S, Torigoe K, Tanimoto T, Okamura H, Kunikata T;  
XX PI Taniguchi M, Kohno K, Fukuda S, Kurimoto M;  
XX WPI; 1996-252837/26.  
XX DR N-PSDB; AAT32404.  
XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful to  
XX treat and prevent, e.g. viral disease, malignancies and immune disorders.  
XX Claim 6; Page 41-42; 48pp; English.  
XX The mature portion of a novel human protein (AAR99560) induces interferon  
XX -gamma (IFN-gamma) prodn. by immunocompetent cells. It is the product of  
XX a cDNA clone (AAT32404) obtd. from a human liver library. The protein  
XX enhances the cytotoxicity of killer cells and/or induces the formation of  
XX killer cells (e.g. NK cells, lymphokine-activating killer (LAK) cells,  
XX and cytotoxic T-cells). The mature protein (see also AAR99558) is useful  
XX as an antiviral, antitumor, antibacterial, immunoregulatory and blood  
XX platelet enhancing agent, and can be used in adoptive immunotherapy. It  
XX is also used to raise monoclonal antibodies  
XX Sequence 193 AA;

Query Match 99.4%; Score 156; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. 2.5e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIIFIISMYKDSQPRGM 60  
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIIFIISMYKDSQPRGM 96  
QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120  
DB 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193  
RESULT 14  
AAW52172  
ID AAW52172 standard; peptide; 193 AA.  
XX AC AAW52172;  
XX DT 10-JUN-1998 (first entry)  
XX DE Interferon-gamma inducing polypeptide precursor sequence.  
XX DE Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT FT Misc-difference 109  
FT FT /label= Ile, Thr  
XX EP819757-A2.  
XX PD 21-JAN-1998.  
XX PF 18-JUL-1997; 97EP-00305377.  
XX PR 19-JUL-1996; 96JP-00207691.  
XX PR 30-MAY-1997; 97JP-00156062.  
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX PI Tanimoto T, Kurimoto M;  
XX WPI; 1998-078838/08.  
XX DR N-PSDB; AAV17200.  
XX Polypeptide-processing enzyme - for preparing mature form of interferon-  
XX inducing polypeptide.  
XX Claim 3; Page 15; 18pp; English.  
XX This sequence represents the precursor of an interferon-gamma (IFN-gamma)  
XX inducing polypeptide. The polypeptide induces IFN-gamma production in  
XX immunocompetent cells [the polypeptide is not named but is described in  
XX JP 27198/96 and 193098/96]. An enzyme can convert this precursor form  
XX into its active form by cleaving a linkage between Asp at amino acid  
XX position 36 and Tyr at amino acid position 37 of its N-terminal fragment.  
XX The enzyme can be obtained from a human haematopoietic cell and can be  
XX inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-aspart  
XX -1-al. The enzyme can be used for cleaving a recombinant IFN-gamma pro-  
XX polypeptide to form a mature polypeptide  
XX Sequence 193 AA;  
Query Match 99.4%; Score 156; DB 2; Length 193;  
Best Local Similarity 100.0%; Pred. No. 2.5e-162;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
 Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 96  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 120  
 Db 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 156  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
 Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193  
 RESULT 15  
 AAW47429  
 ID AAW47429 standard; protein; 193 AA.  
 AC AAW47429;  
 XX  
 DT 05-JUN-1998 (first entry)  
 XX  
 DE Interferon-gamma production inducer.  
 XX  
 KW Interferon-gamma; IFN-gamma; production inducer; gene therapy;  
 KW immunocompetent cell; treatment; prevention; malignant tumour;  
 KW viral infection; bacterial infection; immune disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..36  
 FT Peptide /label= sig\_peptide  
 FT Peptide 37..193  
 FT Peptide /label= mat\_peptide  
 FT Misc-difference 109  
 FT /label= Ile, Thr  
 XX  
 PN EP016499-A2.  
 XX  
 XX 07-JAN-1998.  
 PD  
 PF 27-JUN-1997; 97EP-00304616.  
 XX  
 PR 27-JUN-1996; 96JP-00185305.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 PI Okura T, Torigoe K, Kurimoto M;  
 XX  
 XX WPI; 1998-054914/06.  
 DR N-PSDB; AAV15825, AAV15826.  
 XX  
 XX Genomic DNA encoding polypeptide inducing interferon-gamma production -  
 PT by immuno-competent cells, useful to treat e.g. human malignant tumours  
 PT or viral diseases.  
 XX  
 PS Claim 2; Page 49-50; 74pp; English.  
 XX  
 CC The present sequence is a protein, which induces interferon-gamma (IFN-  
 CC gamma) production in immunocompetent cells. The protein has high  
 CC biological activity, including enhancing cytotoxicity of killer cells and  
 CC inducing killer cell formation, in addition to inducing IFN-gamma  
 CC production by immunocompetent cells when expressed in mammalian cells,  
 CC facilitating its use in low dosages to treat/prevent, e.g. malignant  
 CC tumours, viral or bacterial infections and immune diseases. As it is  
 CC expressed in mammalian cells, it also has low toxicity when used in human  
 CC treatments, minimising side effects. The DNA encoding the protein can be  
 CC used in gene therapy, e.g. by injecting vectors containing the DNA or  
 CC transplanting cells  
 XX  
 SQ Sequence 193 AA;

Query Match 99.4%; Score 156; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 60  
 Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNDNAPRTIFIISMYKDSQPRGM 96  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 120  
 Db 97 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSIIFFQRSVPGHDKMQPESSSY 156  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
 Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193  
 RESULT 16  
 AAW37740  
 ID AAW37740 standard; protein; 193 AA.  
 XX  
 AC AAW37740;  
 XX  
 DT 07-JUL-1998 (first entry)  
 XX  
 DE Interferon-gamma inducing precursor peptide.  
 KW Interferon-gamma inducing precursor peptide; IFN-gamma;  
 KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;  
 KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.  
 XX  
 OS Mammalia.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 36..157  
 FT /notes= "Mature protein"  
 FT Cleavage-site 36..37  
 FT Misc-difference 109  
 FT /label= Ile, Thr  
 XX  
 PN EP821005-A2.  
 XX  
 XX 28-JAN-1998.  
 PD  
 PF 18-JUL-1997; 97EP-00305376.  
 XX  
 PR 25-JUL-1996; 96JP-00213267.  
 PR 31-JAN-1997; 97JP-00031474.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 XX Tanimoto T, Kurimoto M;  
 XX  
 XX WPI; 1998-088847/09.  
 DR N-PSDB; AAV18906.  
 XX  
 XX Conversion of interferon-inducing polypeptide precursor to active  
 PT polypeptide - comprises use of interferon-1-beta-converting enzyme,  
 PT useful for, e.g. enhancing cytotoxicity by killer cells.  
 XX  
 PS Claim 2; Page 14-15; 18pp; English.  
 XX  
 CC This is the amino acid sequence for the interferon-gamma (IFN-gamma)  
 CC inducing precursor peptide, which is cleaved to form the active mature  
 CC protein when it is in contact with interleukin-1-beta-converting enzyme  
 CC (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma  
 CC a useful biologically active substance, enhancing cytotoxicity by, and  
 CC inducing the formation of killer cells. The polypeptide may potentially  
 CC be used as an antiviral, antitumour and immunopathy agent and as an  
 CC antiseptic  
 XX  
 SQ Sequence 193 AA;

```
Query Match      99.4%; Score 156; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 120
DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 17
AAV53908
ID AAV53908 standard; protein; 193 AA.
XX
AC AAV53908;
XX
DT 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of a protein that induces IFN-gamma production.
XX
KW Human; interferon gamma production; IFN-gamma; immunocompetent cell;
KW antiviral; immunoregulatory; antigen; mitogen;
KW IFN-gamma susceptible disease; antibacterial; antitumour;
KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;
KW AIDS; bacterial disease; Candidiasis; malaria; solid malignant tumour;
KW renal cancer; mycosis fungoides; chronic granulomatous disease;
KW blood cell malignant tumour; adult T cell leukaemia;
KW chronic myelogenous leukaemia; malignant leukaemia;
KW immune disease allergy; rheumatism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..36 /note= "signal peptide"
FT Protein 37..193 /note= "mature protein"
FT Misc-difference 109 /label= Ile, Thr
FT /note= "encoded by AYT"
XX
PN EP962531-A2.
XX
PD 08-DEC-1999.
XX
PF 10-NOV-1995; 99EP-00104104.
XX
PR 15-NOV-1994; 94JP-00304203.
PR 23-FEB-1995; 95JP-00058240.
PR 10-MAR-1995; 95JP-00078357.
PR 18-SEP-1995; 95JP-00262062.
PR 29-SEP-1995; 95JP-00274988.
PR 10-NOV-1995; 95EP-00308055.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Ushio S, Torigoe K, Tanimoto T, Okamura H;
XX
DR WPI; 2000-064289/06.
DR N-PSDB; AA236876.
XX
PT Novel polypeptides used in the treatment of interferon-gamma susceptible diseases.
PS Example A-4-3; Page 7; 42pp; English.
XX
```

```
CC The present sequence represents a human protein that induces interferon
CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a protein
CC which has antiviral, antitumour and immunoregulatory activities, and is
CC produced by immunocompetent cells stimulated with antigens or mitogens.
CC The protein of the invention is used to treat IFN-gamma susceptible
CC diseases, and also have use as a antiviral agent, antibacterial agent,
CC antitumour agent, immunoregulatory agent and blood platelet enhancing
CC agent. Diseases which can be treated with the protein include viral
CC diseases such as hepatitis, herpes syndrome, condyloma, and AIDS;
CC bacterial diseases such as Candidiasis and malaria; solid malignant
CC tumours such as renal cancer, mycosis fungoides, and chronic
CC granulomatous disease; blood cell malignant tumours such as adult T cell
CC leukaemia, chronic myelogenous leukaemia, and malignant leukaemia; and
CC immune diseases such as allergy and rheumatism
XX
SQ Sequence 193 AA;

Query Match      99.4%; Score 156; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.5e-162;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 120
DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHNDKMQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 18
AAB82409
ID AAB82409 standard; protein; 193 AA.
XX
AC AAB82409;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human interleukin-18 precursor.
XX
KW Interleukin-18; antibody; human; infection; tumour; sarcoma;
KW autoimmune disease; therapy; diagnosis; detoxification.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..36 /label= Signal_peptide
FT Protein 37..193 /label= Mature_protein
FT Misc-difference 109 /label= Ile, Thr
XX
PN EP1101772-A1.
XX
PD 23-MAY-2001.
XX
PF 15-NOV-2000; 2000EP-00310121.
XX
PR 16-NOV-1999; 99JP-00324860.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Tohru K, Taniguchi M, Yamauchi H, Kurimoto M;
XX
DR WPI; 2001-368892/39.
DR N-PSDB; AAF90444.
XX
PT New antibodies specific to interleukin 18 (IL-18) precursor, useful in
```

PT manufacturing a medicament for treating IL-18-related diseases, e.g.  
 PT autoimmune disease, or for detecting, eliminating or detoxifying the  
 PT precursor.

XX Example 1-2; Page 14-15; 27pp; English.

XX The present sequence is that of human interleukin-18 (IL-18) precursor.  
 CC Monoclonal and polyclonal antibodies specific to the human IL-18  
 CC precursor propeptide (see AB82406) are claimed. These are useful in  
 CC detection and purification of IL-18 precursor, and in the elimination and  
 CC detoxification of the precursor accumulated in vivo. Detection methods  
 CC using the antibody are effective in qualitative and quantitative analyses  
 CC for the precursor, and also in the correction of imprecise results  
 CC obtained from assays using anti-IL-18 antibody, which exhibit cross-  
 CC reactivity against the precursor. Pharmaceutical compositions comprising  
 CC an antibody specific to the IL-18 precursor can be used to treat viral  
 CC infections including AIDS, bacterial infections, solid malignant tumours,  
 CC malignant tumours of haemocytes, sarcomas, autoimmune disease,  
 CC hepatopathy, pancreatopathy, and diseases of the gallbladder, kidney and  
 CC nervous system. Detection methods using the antibody can be used to  
 CC diagnose such diseases.

XX Sequence 193 AA;

Query Match 99.4%; Score 156; DB 4; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96  
 QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSEY 120  
 DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSEY 156  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
 DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 19

ADL24278  
 ID ADL24278 standard; protein; 193 AA.  
 XX  
 AC ADL24278;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human IL-18.  
 XX  
 KW cardiovascular disease; IL-17; interleukin; IL-18; 4-1BB; CD30; OX40;  
 KW antagonist.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004019866-A2.  
 XX  
 PD 11-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-US026354.  
 XX  
 PR 28-AUG-2002; 2002US-0406418P.  
 PR 12-AUG-2003; 2003US-0494457P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Burton PB, Deisher TA;  
 XX  
 DR WPI; 2004-239107/22.  
 DR N-PSDB; ADL24277.  
 XX  
 PT Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a

PT cardiovascular disease, e.g. chronic immune myocarditis, congestive heart  
 PT failure, aneurysm, angina, embolism, restenosis, ischemia or  
 PT thrombocytopenic purpura.

XX Disclosure; Page 111-112; 135pp; English.

XX The present invention relates to a method of treating cardiovascular  
 CC disease in a subject, comprising administering an IL-17, IL-18, 4-1BB,  
 CC CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40  
 CC antagonists are useful for treating cardiovascular disorders, e.g.  
 CC (chronic immune) myocarditis, congestive heart failure, aneurysms,  
 CC angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The  
 CC present sequence is a polypeptide used in the exemplification of the  
 CC invention.

XX Sequence 193 AA;

Query Match 99.4%; Score 156; DB 8; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-162;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96  
 QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSEY 120  
 DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKMQPESSEY 156  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
 DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 20

AAW77084  
 ID AAW77084 standard; peptide; 157 AA.  
 XX  
 AC AAW77084;  
 XX  
 DT 16-NOV-1998 (first entry)  
 XX  
 DE Human interleukin 18 derivative 2.  
 XX  
 KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
 KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
 KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.  
 XX  
 OS Homo sapiens.  
 XX  
 FN EP861663-A2.  
 XX  
 PD 02-SEP-1998.  
 XX  
 PF 24-FEB-1998; 98EP-00301352.  
 XX  
 PR 25-FEB-1997; 97JP-00055468.  
 XX  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 XX  
 PI Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;  
 XX  
 DR WPI; 1998-448964/39.  
 XX  
 PT Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
 PT e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
 PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism  
 PT and osteoporosis.  
 XX  
 PS Disclosure; Page 30-31; 56pp; English.  
 XX  
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for  
 CC inhibition of osteoclast formation. IL-18 is used for treating or

CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
CC osteoporosis  
XX  
SQ Sequence 157 AA;

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.9e-83;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
DB 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKLILKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 21

AAW77077  
ID AAW77077 standard; peptide; 157 AA.

XX  
AC AAW77077;  
DT 16-NOV-1998 (first entry)  
DE Human interleukin 18.

XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.  
XX Homo sapiens.

XX EP861663-A2.  
XX 02-SEP-1998.

XX 24-FEB-1998; 98EP-00301352.  
XX 25-FEB-1997; 97JP-00055468.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;

XX WPI; 1998-448964/39.  
XX N-PSDB; AAV48226.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
PT e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism  
PT and osteoporosis.

XX Claim 4; Page 18; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for  
CC inhibition of osteoclast formation. IL-18 is used for treating or  
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
CC osteoporosis  
XX

SQ Sequence 157 AA;

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.9e-83;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
DB 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

DB 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
QY 134 FKLILKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 22

AAW77083  
ID AAW77083 standard; peptide; 157 AA.

XX  
AC AAW77083;  
DT 16-NOV-1998 (first entry)

XX Human interleukin 18 derivative 1.

XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.  
XX Homo sapiens.

XX EP861663-A2.  
XX 02-SEP-1998.

XX 24-FEB-1998; 98EP-00301352.  
XX 25-FEB-1997; 97JP-00055468.

XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;

XX WPI; 1998-448964/39.  
XX Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
PT e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
PT chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism  
PT and osteoporosis.

XX Disclosure; Page 30; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for  
CC inhibition of osteoclast formation. IL-18 is used for treating or  
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
CC osteoporosis  
XX

SQ Sequence 157 AA;

Query Match 53.5%; Score 84; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.9e-83;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133  
DB 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNEED 157  
DB 134 FKLILKKEDELGDRSIMFTVQNEED 157

## RESULT 23

AAW48961  
ID AAW48961 standard; peptide; 157 AA.

XX  
AC AAW48961;  
DT 25-SEP-1998 (first entry)

```

XX DE Mutant human interferon-gamma inducing factor IGIF/MUT12.
XX KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
XX KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
OS Homo sapiens.
OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 68
XX FT /note= "changed from Cys in wild-type to Ser in mutant"
XX PN EP845530-A2..
XX PD 03-JUN-1998.
XX PF 28-NOV-1997; 97EP-00309632.
XX PR 29-NOV-1996; 96JP-00333037.
XX PR 21-JAN-1997; 97JP-00020906.
XX PR 14-NOV-1997; 97JP-00329715.
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI Yamamoto K, Okamoto I, Kurimoto M;
XX DR WPI; 1998-288747/26.
XX DR N-PSDB; AAV32625.
XX FT Mutants of interferon-gamma inducing polypeptide - useful as antitumour,
XX FT antiviral, antimicrobial or anti-immunopathic agents.
XX PS Claim 5; Page 41; 59pp; English.
XX CC The present sequence represents the mutant human interferon-gamma
XX CC inducing factor IGIF/MUT12. The wild-type human interferon-gamma factor
XX CC sequence is shown in AAW48959. The invention provides for mutant human
XX CC and mouse interferon-gamma inducing factors (IGIF) in which one or more
XX CC cysteine residues are replaced with different residues at or away from
XX CC the consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
XX CC capable of stimulating immunocompetent cells for the production of
XX CC interferon-gamma and are claimed to be less toxic, more active and stable
XX CC than the corresponding wild type interferon-gamma inducing factor. The
XX CC mutant IGIFs are also claimed to enhance killer cell cytotoxicity and/or
XX CC induce killer cell formation, and may therefore be useful as antitumour
XX CC agents, antitumour immunotherapeutics, antiviral agents and antimicrobial
XX CC agents. The mutant IGIFs are also claimed to be useful for treating
XX CC hepatitis, acquired immunodeficiency syndrome (AIDS), malaria,
XX CC tuberculosis, solid malignant tumours (e.g. renal carcinoma), rheumatism,
XX CC osteoporosis and thrombopenia caused by radiation- and chemo-therapy
XX SQ Sequence 157 AA;
Query Match 53.5%; Score 84; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKNQMFESSYEGYFLACEKRD 133
DB 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKNQMFESSYEGYFLACEKRD 133
QY 134 FKLLKKEDELGDRSIMFTVQNE 157
DB 134 FKLLKKEDELGDRSIMFTVQNE 157
RESULT 24
AAW48962
ID AAW48962 standard; peptide; 157 AA.
XX

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```

AC AAW48962;
XX 25-SEP-1998 (first entry)
XX Mutant human interferon-gamma inducing factor IGIF/MUT21.
XX Interferon-gamma inducing factor; interferon-gamma; killer cell;
XX KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 38
XX FT /note= "changed from Cys in wild-type to Ser in mutant"
XX PN EP845530-A2.
XX PD 03-JUN-1998.
XX PF 28-NOV-1997; 97EP-00309632.
XX PR 29-NOV-1996; 96JP-00333037.
XX PR 21-JAN-1997; 97JP-00020906.
XX PR 14-NOV-1997; 97JP-00329715.
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI Yamamoto K, Okamoto I, Kurimoto M;
XX DR WPI; 1998-288747/26.
XX DR N-PSDB; AAV32626.
XX FT Mutants of interferon-gamma inducing polypeptide - useful as antitumour,
XX FT antiviral, antimicrobial or anti-immunopathic agents.
XX PS Claim 5; Page 41; 59pp; English.
XX CC The present sequence represents the mutant human interferon-gamma
XX CC inducing factor IGIF/MUT21. The wild-type human interferon-gamma factor
XX CC sequence is shown in AAW48959. The invention provides for mutant human
XX CC and mouse interferon-gamma inducing factors (IGIF) in which one or more
XX CC cysteine residues are replaced with different residues at or away from
XX CC the consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
XX CC capable of stimulating immunocompetent cells for the production of
XX CC interferon-gamma and are claimed to be less toxic, more active and stable
XX CC than the corresponding wild type interferon-gamma inducing factor. The
XX CC mutant IGIFs are also claimed to enhance killer cell cytotoxicity and/or
XX CC induce killer cell formation, and may therefore be useful as antitumour
XX CC agents, antitumour immunotherapeutics, antiviral agents and antimicrobial
XX CC agents. The mutant IGIFs are also claimed to be useful for treating
XX CC hepatitis, acquired immunodeficiency syndrome (AIDS), malaria,
XX CC tuberculosis, solid malignant tumours (e.g. renal carcinoma), rheumatism,
XX CC osteoporosis and thrombopenia caused by radiation- and chemo-therapy
XX SQ Sequence 157 AA;
Query Match 53.5%; Score 84; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKNQMFESSYEGYFLACEKRD 133
DB 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKNQMFESSYEGYFLACEKRD 133
QY 134 FKLLKKEDELGDRSIMFTVQNE 157
DB 134 FKLLKKEDELGDRSIMFTVQNE 157
RESULT 25

```

AAAY57570  
ID AAAY57570 standard; protein; 157 AA.  
XX  
AC AAAY57570;  
XX  
DT 06-MAR-2000 (first entry)  
XX  
DE Human interleukin 18 protein sequence SEQ ID NO:1.  
XX  
KW Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;  
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO959565-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US011160.  
XX  
PR 21-MAY-1998; 98US-0086560P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Johnson RK;  
XX  
DR WPI; 2000-062368/05.  
XX  
PT New polypeptides, useful for preparation of composition for preventing  
PT and/or treating cancer by inhibiting tumor growth.  
XX  
PS Claim 1; Page 49-50; 53pp; English.  
XX  
CC The present sequence represents human interleukin 18 (IL-18). The present  
CC invention describes a compound comprising human or murine IL-18 in  
CC combination with a chemotherapeutic agent (I). Also described are: (1) a  
CC method of preventing and/or treating cancer in a mammal comprising the  
CC administration of a cancer inhibiting amount of (I) comprising the IL-18  
CC protein and the chemotherapeutic agent and optionally a pharmaceutically  
CC acceptable carrier; and (2) a method of inhibiting the growth of tumour  
CC cells in a mammal sensitive to a composition comprising human IL-18  
CC and/or murine IL-18 and the chemotherapeutic agent (and optionally a  
CC pharmaceutically acceptable carrier), comprising administering to a  
CC mammal afflicted with the tumour cells an effective tumour cell growth  
CC inhibiting amount of (I). The IL-18 protein in conjunction with a  
CC chemotherapeutic agent is useful in a method for preventing and/or  
CC treating cancer in mammals by inhibiting the growth of tumours or  
CC cancerous cells in mammals  
XX  
SQ Sequence 157 AA;  
  
Query Match 53.5%; Score 84; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.9e-83;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 74 LSCENKIIISFKENPPDNIDKTKSDIIFQRSVPGHDKMKQFESSYEGYFLACEKERDL 133  
DB 74 LSCENKIIISFKENPPDNIDKTKSDIIFQRSVPGHDKMKQFESSYEGYFLACEKERDL 133  
  
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Job time : 135 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:58:16 ; Search time 116 Seconds  
(without alignments)  
565.510 Million cell updates/sec

Title: US-09-716-356A-6  
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Minimum DB seq length: 0  
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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2	156	99.4	157 3 US-09-752-510-6 Sequence 6, Appli
3	156	99.4	157 3 US-09-924-099-21 Sequence 21, Appli
4	156	99.4	157 4 US-10-327-089-1 Sequence 1, Appli
5	156	99.4	157 4 US-10-349-023-26 Sequence 26, Appli
6	156	99.4	157 5 US-10-730-034-1 Sequence 1, Appli
7	156	99.4	193 4 US-10-646-308-13 Sequence 13, Appli
8	84	53.5	157 3 US-09-775-046-9 Sequence 9, Appli
9	84	53.5	157 3 US-09-030-061-6 Sequence 6, Appli
10	84	53.5	157 3 US-09-030-061-20 Sequence 20, Appli
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14	84	53.5	157 4 US-10-100-057-21 Sequence 21, Appli
15	84	53.5	157 4 US-10-094-153-2 Sequence 2, Appli
16	84	53.5	157 4 US-10-094-153-6 Sequence 6, Appli
17	84	53.5	157 4 US-10-094-153-7 Sequence 7, Appli
18	84	53.5	157 4 US-10-094-153-8 Sequence 8, Appli
19	84	53.5	157 4 US-10-094-153-10 Sequence 10, Appli
20	84	53.5	157 4 US-10-260-576-4 Sequence 4, Appli
21	84	53.5	157 4 US-10-260-576-6 Sequence 6, Appli
22	84	53.5	157 4 US-10-260-576-7 Sequence 7, Appli
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24	84	53.5	157 4 US-10-311-491-3 Sequence 3, Appli
25	84	53.5	157 4 US-10-105-080-10 Sequence 10, Appli
26	84	53.5	157 4 US-10-397-786A-3 Sequence 3, Appli
27	84	53.5	157 4 US-10-280-576-1 Sequence 1, Appli

28	84	53.5	157 4 US-10-646-308-14 Sequence 14, Appli
29	84	53.5	157 5 US-10-872-198-98 Sequence 98, Appli
30	84	53.5	157 5 US-10-823-964A-1 Sequence 1, Appli
31	84	53.5	157 5 US-10-823-964A-4 Sequence 4, Appli
32	84	53.5	157 5 US-10-666-490A-1 Sequence 1, Appli
33	84	53.5	157 5 US-10-518-331-1 Sequence 1, Appli
34	84	53.5	157 6 US-11-021-951-98 Sequence 98, Appli
35	84	53.5	158 4 US-10-695-195-7 Sequence 7, Appli
36	84	53.5	158 4 US-10-694-978-7 Sequence 7, Appli
37	84	53.5	193 3 US-09-798-075-1 Sequence 1, Appli
38	84	53.5	193 3 US-09-770-528-8 Sequence 8, Appli
39	84	53.5	193 4 US-10-094-153-3 Sequence 3, Appli
40	84	53.5	193 4 US-10-094-153-4 Sequence 4, Appli
41	84	53.5	193 4 US-10-094-153-5 Sequence 5, Appli
42	84	53.5	193 4 US-10-094-153-9 Sequence 9, Appli
43	84	53.5	193 4 US-10-311-491-1 Sequence 1, Appli
44	84	53.5	193 4 US-10-105-080-4 Sequence 4, Appli
45	84	53.5	193 4 US-10-679-201-5 Sequence 5, Appli
46	84	53.5	193 5 US-10-706-689-1 Sequence 1, Appli
47	84	53.5	193 5 US-10-988-360-1 Sequence 1, Appli
48	84	53.5	203 5 US-10-823-964A-3 Sequence 3, Appli
49	84	53.5	233 4 US-10-311-491-10 Sequence 10, Appli
50	84	53.5	325 5 US-10-895-396-10 Sequence 10, Appli
51	84	53.5	325 5 US-10-895-396-11 Sequence 11, Appli
52	84	53.5	361 5 US-10-895-396-8 Sequence 8, Appli
53	84	53.5	361 5 US-10-895-396-9 Sequence 9, Appli
54	83	52.9	157 5 US-10-823-964A-8 Sequence 8, Appli
55	83	52.9	157 5 US-10-823-964A-10 Sequence 10, Appli
56	81	51.6	157 3 US-09-030-061-25 Sequence 25, Appli
57	81	51.6	157 4 US-10-100-057-25 Sequence 25, Appli
58	81	51.6	157 4 US-10-280-576-11 Sequence 11, Appli
59	79	50.3	157 5 US-10-823-964A-5 Sequence 5, Appli
60	72	45.9	156 4 US-10-414-774-1 Sequence 1, Appli
61	70	44.6	157 5 US-10-823-964A-7 Sequence 7, Appli
62	70	44.6	157 5 US-10-823-964A-9 Sequence 9, Appli
63	67	42.7	157 3 US-09-030-061-22 Sequence 22, Appli
64	67	42.7	157 4 US-10-100-057-22 Sequence 22, Appli
65	67	42.7	157 4 US-10-280-576-8 Sequence 8, Appli
66	53	33.8	157 3 US-09-030-061-23 Sequence 23, Appli
67	53	33.8	157 4 US-10-100-057-23 Sequence 23, Appli
68	53	33.8	157 4 US-10-260-576-9 Sequence 9, Appli
69	50	31.8	157 3 US-09-752-510-2 Sequence 2, Appli
70	50	31.8	157 3 US-09-030-061-24 Sequence 24, Appli
71	50	31.8	157 3 US-09-030-061-26 Sequence 26, Appli
72	50	31.8	157 4 US-10-100-057-24 Sequence 24, Appli
73	50	31.8	157 4 US-10-100-057-26 Sequence 26, Appli
74	50	31.8	157 4 US-10-260-576-10 Sequence 10, Appli
75	50	31.8	157 4 US-10-260-576-12 Sequence 12, Appli
76	47	29.9	157 5 US-10-823-964A-6 Sequence 6, Appli
77	26	16.6	26 5 US-10-823-964A-14 Sequence 14, Appli
78	17	10.8	17 3 US-09-752-510-5 Sequence 5, Appli
79	17	10.8	17 3 US-09-030-061-13 Sequence 13, Appli
80	17	10.8	17 4 US-10-100-057-13 Sequence 13, Appli
81	17	10.8	17 5 US-10-823-964A-24 Sequence 24, Appli
82	14	8.9	14 3 US-09-752-510-4 Sequence 4, Appli
83	14	8.9	14 3 US-09-030-061-12 Sequence 12, Appli
84	14	8.9	14 4 US-10-100-057-12 Sequence 12, Appli
85	13	8.3	13 3 US-09-752-510-7 Sequence 7, Appli
86	13	8.3	13 3 US-09-030-061-11 Sequence 11, Appli
87	13	8.3	13 4 US-10-100-057-11 Sequence 11, Appli
88	13	8.3	13 3 US-09-917-265-5 Sequence 5, Appli
89	13	8.3	154 5 US-10-821-670-5 Sequence 5, Appli
90	13	8.3	157 5 US-09-917-265-12 Sequence 12, Appli
91	13	8.3	157 5 US-10-821-670-12 Sequence 12, Appli
92	13	8.3	192 3 US-09-917-265-8 Sequence 8, Appli
93	13	8.3	192 5 US-10-821-670-8 Sequence 8, Appli
94	10	6.4	10 3 US-09-752-510-1 Sequence 1, Appli
95	10	6.4	10 3 US-09-752-510-3 Sequence 3, Appli
96	10	6.4	10 3 US-09-030-061-10 Sequence 10, Appli
97	10	6.4	10 3 US-09-030-061-15 Sequence 15, Appli
98	10	6.4	10 4 US-10-100-057-10 Sequence 10, Appli
99	10	6.4	10 4 US-10-100-057-15 Sequence 15, Appli
100	10	6.4	10 4 US-10-280-576-27 Sequence 27, Appli



## ALIGNMENTS

## RESULT 1

US-08-996-140-1  
; Sequence 1, Application US/08996140  
; Publication No. US20030190318A1  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: USHIO, Shimpel  
; APPLICANT: KUNIKATA, Toshio  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,140  
; FILING DATE: 22-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 356,426/1996  
; FILING DATE: 26-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 52,526/1997  
; FILING DATE: 21-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 163,490/1997  
; FILING DATE: 6-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 215,490/1997  
; FILING DATE: 28-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE=2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-996-140-1

Query Match 99.4%; Score 156; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	YFGKLESKSLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIIFISMYKDSQPRGM	60
DB	1	YFGKLESKSLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIIFISMYKDSQPRGM	60
QY	61	AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY	120
DB	61	AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY	120
QY	121	EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE	157
DB	121	EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE	157

## RESULT 2

US-09-752-510-6  
; Sequence 6, Application US/09752510  
; Publication No. US20010018212A1  
; GENERAL INFORMATION:  
; APPLICANT: AKITA, Kenji  
; NUKADA, Yoshiyuki  
; FUJII, Mitsukiyo  
; TANIMOTO, Tadao  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA  
; PRODUCTION BY IMMUNOCOMPETENT CELL  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/752,510  
; FILING DATE: 03-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/721,018  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: JP 96-067434  
; FILING DATE: 29-FEB-1996  
; APPLICATION NUMBER: JP not yet received  
; FILING DATE: 20-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: AKITA=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: "Xaa" in position 73 is either  
; 'ile' or 'Thr'  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-752-510-6

Query Match 99.4%; Score 156; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.4e-147;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	YFGKLESKSLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIIFISMYKDSQPRGM	60
DB	1	YFGKLESKSLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIIFISMYKDSQPRGM	60
QY	61	AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY	120
DB	61	AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY	120
QY	121	EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE	157
DB	121	EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE	157

```
RESULT 3
US-09-924-099-21
; Sequence 21, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 21
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (73)
; OTHER INFORMATION: "Xaa" means an amino acid of isoleucine or threonine.
US-09-924-099-21

Query Match          99.4%; Score 156; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKTKSDIIFQFQSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKTKSDIIFQFQSVPGHNDKMQFESSY 120

Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157

RESULT 4
US-10-327-069-1
; Sequence 1, Application US/10327069
; Publication No. US20030129184A1
; GENERAL INFORMATION:
; APPLICANT: KENKYUJO
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION NUMBER: US/10/349,023
; FILING DATE: 23-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,972
; FILING DATE: 24-Apr-2000
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997

SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/327,069
FILING DATE: 24-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE: No. US20030129184A1ember 15, 1995
APPLICATION NUMBER: JP 58,240/95
FILING DATE: February 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-327-069-1

Query Match          99.4%; Score 156; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

Qy 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKTKSDIIFQFQSVPGHNDKMQFESSY 120
Db 61 AVTISVCKEKISXLSCKENKIISFKEMNPPDNIKTKSDIIFQFQSVPGHNDKMQFESSY 120

Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNE 157

RESULT 5
US-10-349-023-26
; Sequence 26, Application US/10349023
; Publication No. US20030133919A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takanori
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,023
; FILING DATE: 23-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,972
; FILING DATE: 24-Apr-2000
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
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; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-730-034-1

Query Match          99.4%; Score 156; DB 5; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
DB      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60

QY      61 AVTISVKCEKISXLSNENKIISPKENMPPNNIKDTKSDIIFQORSVFGHDNKMQFESSY 120
DB      61 AVTISVKCEKISXLSNENKIISPKENMPPNNIKDTKSDIIFQORSVFGHDNKMQFESSY 120

QY      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
US-10-646-308-13
; Sequence 13, Application US/10646308
; Publication No. US20040136992A1
; GENERAL INFORMATION:
; APPLICANT: BURTON, Paul B. J.
; APPLICANT: DEISHER, Theresa A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DIS
; FILE REFERENCE: 3432-B
; CURRENT APPLICATION NUMBER: US/10/646,308
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: --to be assigned--
; PRIOR FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: 60/406,418
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 193.
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: The 'Xaa' at location 73 stands for Thr, or Ile.
US-10-646-308-13

Query Match          99.4%; Score 156; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.7e-147;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 60
DB      37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTFIISMYKDSQPRGM 96

QY      61 AVTISVKCEKISXLSNENKIISPKENMPPNNIKDTKSDIIFQORSVFGHDNKMQFESSY 120
DB      97 AVTISVKCEKISXLSNENKIISPKENMPPNNIKDTKSDIIFQORSVFGHDNKMQFESSY 156

QY      121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB      157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

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RESULT 8
US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-9

Query Match          53.5%; Score 84; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-09-030-061-6
; Sequence 6, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
```

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; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-030-061-6

Query Match          53.5%; Score 84; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133

QY 134 FKLILKKEDELGDRSIMFTVQNE 157
DB 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-09-030-061-20
; Sequence 20, Application US/09030061
; Publication No. US20030095946A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; APPLICANT: HORWOOD, Nicole Joy
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
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Query Match          53.5%; Score 84; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
DB 74 LSCENKIISFKEMNPPDNIKDTSIIFFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
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QY 134 FKLLKKEDELGDRSIMFTVQNE 157  
Db 134 FKLLKKEDELGDRSIMFTVQNE 157

## RESULT 11

US-09-030-061-21  
; Sequence 21, Application US/09030061  
; Publication No. US20030095946A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20030095946A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-030-061-21

Query Match 53.5%; Score 84; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNKDTSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 133  
Db 74 LSCENKIISFKEMNPPDNKDTSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 133  
QY 134 FKLLKKEDELGDRSIMFTVQNE 157  
Db 134 FKLLKKEDELGDRSIMFTVQNE 157

## RESULT 12

US-10-100-057-6  
; Sequence 6, Application US/10100057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20020150555A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT

NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/100,057  
FILING DATE: 19-Mar-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,061  
FILING DATE: 25-FEB-1998  
APPLICATION NUMBER: JP 55,468/1997  
FILING DATE: 25-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GILLISPIE-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6  
Query Match 53.5%; Score 84; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 74 LSCENKIISFKEMNPPDNKDTSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 133  
Db 74 LSCENKIISFKEMNPPDNKDTSDIIFQRSVPGHDKMQFESSYEGYFLACEKERDL 133  
QY 134 FKLLKKEDELGDRSIMFTVQNE 157  
Db 134 FKLLKKEDELGDRSIMFTVQNE 157  
RESULT 13  
US-10-100-057-20  
; Sequence 20, Application US/10100057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, No. US20020150555A1uyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30

;	TELEPHONE: (202) 628-5197	
;	TELEFAX: (202) 737-3528	
;	INFORMATION FOR SEQ ID NO: 21:	
;	SEQUENCE CHARACTERISTICS:	
;	LENGTH: 157 amino acids	
;	TYPE: amino acid	
;	TOPOLOGY: linear	
;	MOLECULE TYPE: peptide	
;	SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
US-10-100-057-21		
Query Match	53.5%; Score 84; DB 4; Length 157;	
Best Local Similarity	100.0%; Pred. No. 1.3e-75;	
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	74 LSCENKIISFKENPPDNIKDTKSDIIFORSVPGHDNKMQFESSSYEGYFLACEKERDL	133
Db	74 LSCENKIISFKENPPDNIKDTKSDIIFORSVPGHDNKMQFESSSYEGYFLACEKERDL	133
QY	134 FKILKKEDELGDRSIMFTVQNE	157
Db	134 FKILKKEDELGDRSIMFTVQNE	157
RESULT 15		
US-10-094-153-2		
;	Sequence 2, Application US/10094153	
;	Publication No. US20020169291A1	
;	GENERAL INFORMATION:	
;	APPLICANT: Dinarello, Charles	
;	APPLICANT: Kim, Soo Hyun	
;	TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use	
;	FILE REFERENCE: 475	
;	CURRENT APPLICATION NUMBER: US/10/094,153	
;	CURRENT FILING DATE: 2002-03-08	
;	PRIOR APPLICATION NUMBER: 60/274,327	
;	PRIOR FILING DATE: 2001-03-08	
;	NUMBER OF SEQ ID NOS: 18	
;	SOFTWARE: Patent in version 3.1	
;	SEQ ID NO 2	
;	LENGTH: 157	
;	TYPE: PRT	
;	ORGANISM: Homo sapiens	
US-10-094-153-2		
Query Match	53.5%; Score 84; DB 4; Length 157;	
Best Local Similarity	100.0%; Pred. No. 1.3e-75;	
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	74 LSCENKIISFKENPPDNIKDTKSDIIFORSVPGHDNKMQFESSSYEGYFLACEKERDL	133
Db	74 LSCENKIISFKENPPDNIKDTKSDIIFORSVPGHDNKMQFESSSYEGYFLACEKERDL	133
QY	134 FKILKKEDELGDRSIMFTVQNE	157
Db	134 FKILKKEDELGDRSIMFTVQNE	157
RESULT 16		
US-10-094-153-6		
;	Sequence 6, Application US/10094153	
;	Publication No. US20020169291A1	
;	GENERAL INFORMATION:	
;	APPLICANT: Dinarello, Charles	
;	APPLICANT: Kim, Soo Hyun	
;	TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use	
;	FILE REFERENCE: 475	
;	CURRENT APPLICATION NUMBER: US/10/094,153	
;	CURRENT FILING DATE: 2002-03-08	
;	PRIOR APPLICATION NUMBER: 60/274,327	
;	PRIOR FILING DATE: 2001-03-08	
;	NUMBER OF SEQ ID NOS: 18	
;	SOFTWARE: Patent in version 3.1	



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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/260,576
  FILING DATE: 01-Oct-2002
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/982,285
  FILING DATE: <Unknown>
  APPLICATION NUMBER: JP 333,037/96
  FILING DATE: No. US20030092130A1ember 29, 1996
  APPLICATION NUMBER: JP 20,906/97
  FILING DATE: January 21, 1997
  APPLICATION NUMBER: JP 10,053,503
  FILING DATE: No. US20030092130A1ember 14, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: BROWDY, Roger L.
  REGISTRATION NUMBER: 25,618
  REFERENCE/DOCKET NUMBER: YAMAMOTO=15
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-628-5197
  TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 157 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match      53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133

Qy 134 FKLILKKEDELGDRSIMFTVQNE 157
Db 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 21
US-10-260-576-6
Sequence 6, Application US/10260576
Publication No. US20030092130A1
GENERAL INFORMATION:
  APPLICANT: YAMAMOTO, Koza
  OKAMOTO, Iwao
  KURIMOTO, Masashi
  TITLE OF INVENTION: POLYPEPTIDES
  NUMBER OF SEQUENCES: 51
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
    STREET: 419 7th Street N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent in Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/260,576
      FILING DATE: 01-Oct-2002
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/982,285
      FILING DATE: <Unknown>
      APPLICATION NUMBER: JP 333,037/96
      FILING DATE: No. US20030092130A1ember 29, 1996
      APPLICATION NUMBER: JP 20,906/97
      FILING DATE: January 21, 1997
      APPLICATION NUMBER: JP 10,053,503
      FILING DATE: No. US20030092130A1ember 14, 1997
    ATTORNEY/AGENT INFORMATION:
      NAME: BROWDY, Roger L.
      REGISTRATION NUMBER: 25,618
      REFERENCE/DOCKET NUMBER: YAMAMOTO=15
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 202-628-5197
        TELEFAX: 202-737-3528
      INFORMATION FOR SEQ ID NO: 4:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 157 amino acids
          TYPE: amino acid
          TOPOLOGY: linear
        MOLECULE TYPE: peptide
        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/260,576
  FILING DATE: 01-Oct-2002
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/982,285
  FILING DATE: <Unknown>
  APPLICATION NUMBER: JP 333,037/96
  FILING DATE: No. US20030092130A1ember 29, 1996
  APPLICATION NUMBER: JP 20,906/97
  FILING DATE: January 21, 1997
  APPLICATION NUMBER: JP 10,053,503
  FILING DATE: No. US20030092130A1ember 14, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: BROWDY, Roger L.
  REGISTRATION NUMBER: 25,618
  REFERENCE/DOCKET NUMBER: YAMAMOTO=15
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-628-5197
  TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 157 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: peptide
  SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-260-576-6

Query Match      53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNKDKSDIIFQSVPGHDKMKQFESSSYEGYFLACEKERDL 133

Qy 134 FKLILKKEDELGDRSIMFTVQNE 157
Db 134 FKLILKKEDELGDRSIMFTVQNE 157

RESULT 22
US-10-260-576-7
Sequence 7, Application US/10260576
Publication No. US20030092130A1
GENERAL INFORMATION:
  APPLICANT: YAMAMOTO, Koza
  OKAMOTO, Iwao
  KURIMOTO, Masashi
  TITLE OF INVENTION: POLYPEPTIDES
  NUMBER OF SEQUENCES: 51
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
    STREET: 419 7th Street N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent in Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/260,576
      FILING DATE: 01-Oct-2002
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/982,285
      FILING DATE: <Unknown>
      APPLICATION NUMBER: JP 333,037/96
      FILING DATE: No. US20030092130A1ember 29, 1996
      APPLICATION NUMBER: JP 20,906/97
      FILING DATE: January 21, 1997
      APPLICATION NUMBER: JP 10,053,503
      FILING DATE: No. US20030092130A1ember 14, 1997
    ATTORNEY/AGENT INFORMATION:
      NAME: BROWDY, Roger L.
      REGISTRATION NUMBER: 25,618
      REFERENCE/DOCKET NUMBER: YAMAMOTO=15
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 202-628-5197
        TELEFAX: 202-737-3528
      INFORMATION FOR SEQ ID NO: 6:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 157 amino acids
          TYPE: amino acid
          TOPOLOGY: linear
        MOLECULE TYPE: peptide
        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-260-576-6
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```
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-260-576-7

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNE 157
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 23
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US2003013292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
; FILE OF INVENTION: IL-18 and IL-18 Combinations
; FILE REFERENCE: P51144
; CURRENT APPLICATION NUMBER: US/10/297,136
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/US01/17924
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNE 157
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 24
US-10-311-491-3
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
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; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; TITLE OF INVENTION: Active IL-18 Polypeptide
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNE 157
Db 134 FKILKKEDELGDRSIMFTVQNE 157

RESULT 25
US-10-105-080-10
; Sequence 10, Application US/10105080
; Publication No. US20030143203A1
; GENERAL INFORMATION:
; APPLICANT: SAMYANG GENEX CORPORATION
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
; TITLE OF INVENTION: GENE THERAPY USING THEM
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/105,080
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: KR 10-2001-78296
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 10
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Human mature inerleukin-18 mutant
US-10-105-080-10

Query Match          53.5%; Score 84; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133
Db 74 LSCENKIISFKEMNPPDNIKDKTSIIFFQSVPGHDNKMQFESSSYEGYFLACEKERDL 133

QY 134 FKILKKEDELGDRSIMFTVQNE 157
Db 134 FKILKKEDELGDRSIMFTVQNE 157

Search completed: January 30, 2006, 09:09:50
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Job time : 117 secs

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